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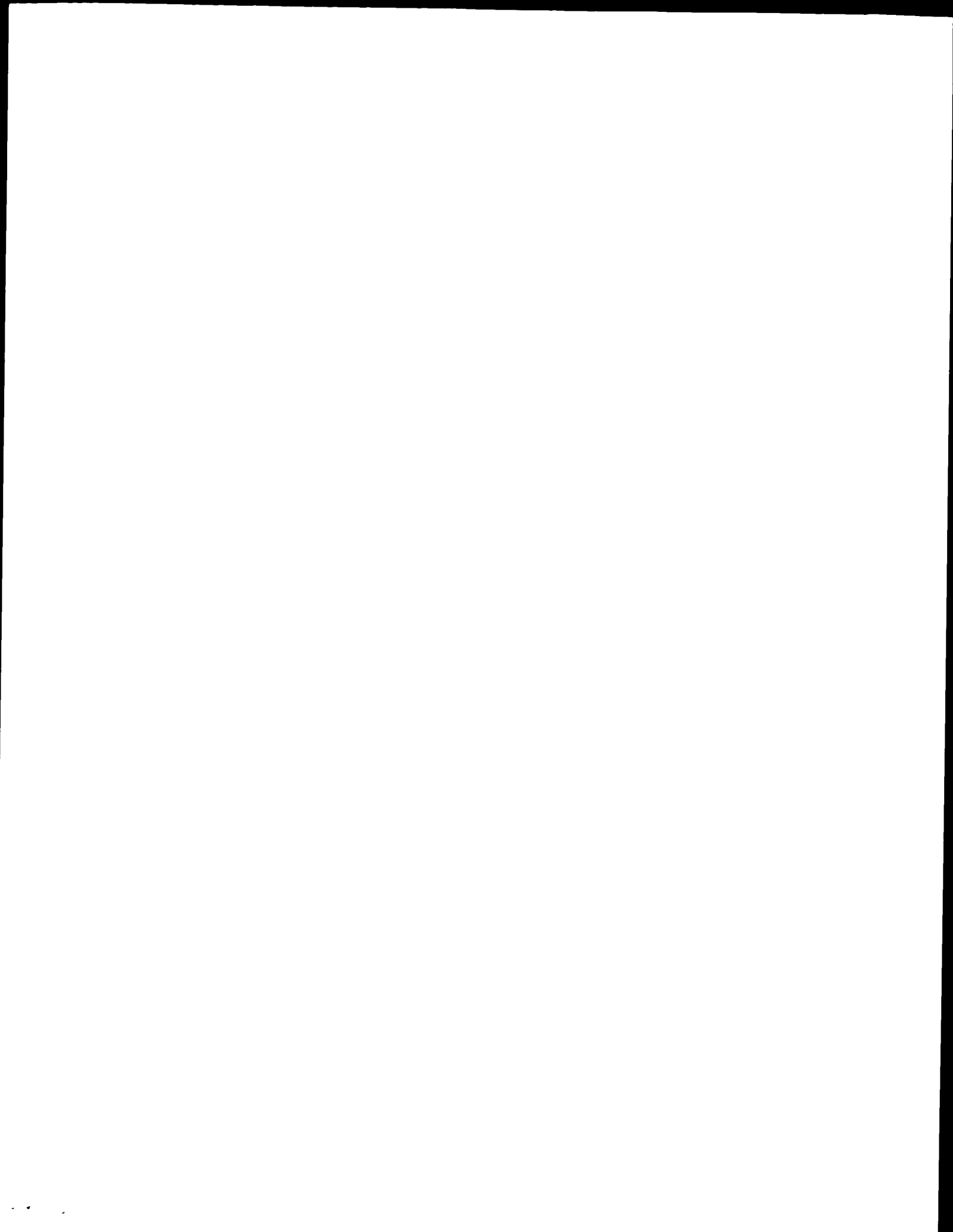
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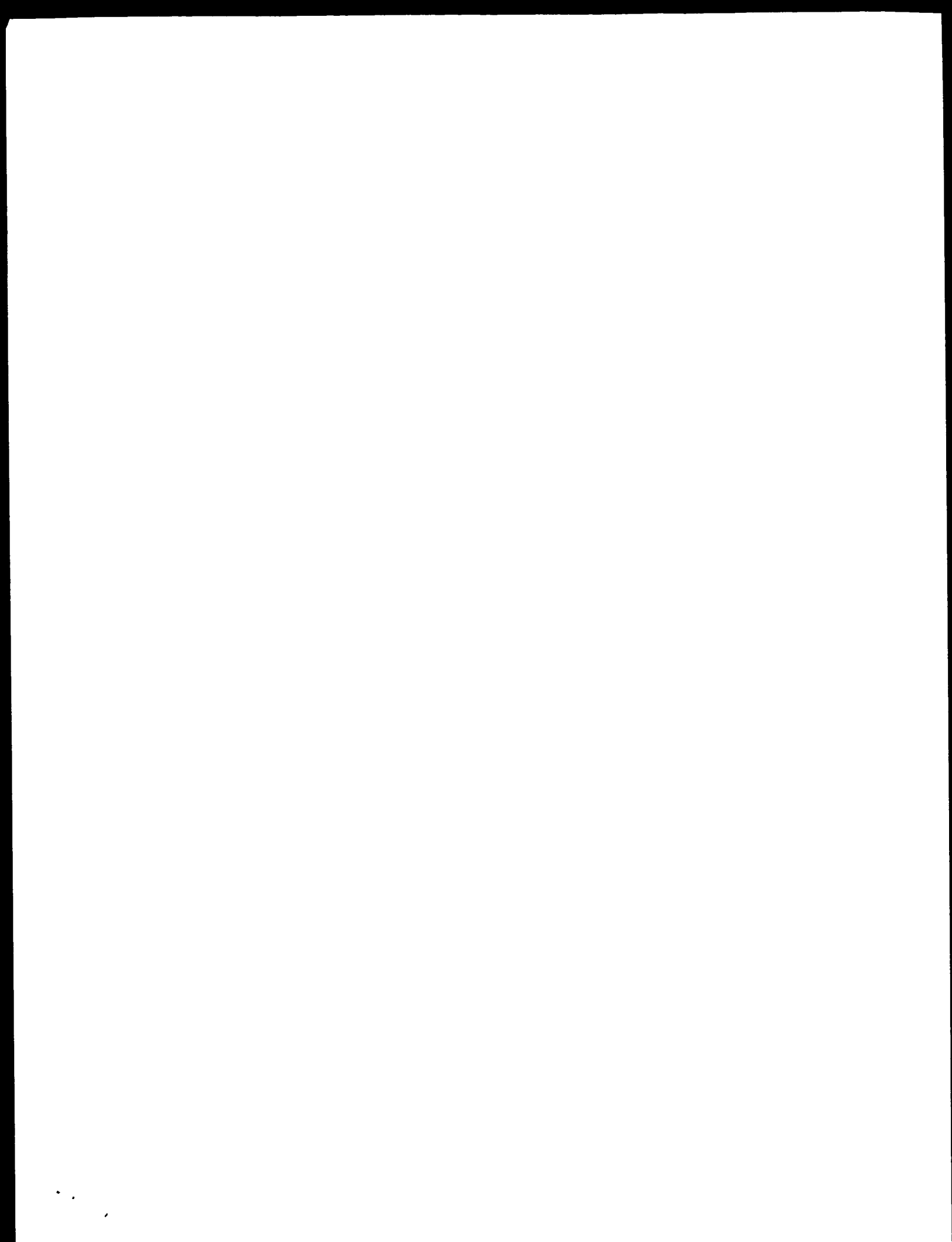
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 Applicant: Eli Lilly
 Applicant: WEL, MIND-HUI
 Applicant: KERRICH, KAREN A.
 Applicant: REASLEY, ELIJAH M.
 Title of Invention: ISOLATED HUMAN TRANSFER PROTEIN,
 Title of Invention: NOVEL ACID NUCLEOTIDES ENCODING HUMAN TRANSFER PROTEINS
 Title of Invention: AND USES THEREOF
 File Reference: 0000651
 Correspondence Number: 09/09/2000 777 770
 Filing Date: 2000-12-04
 Filing Applicant Number: US 60/208,006
 Filing Date: 2000-06-02
 Number of SEQ ID NOS: 3
 Software Package for Windows Version 4.0
 SEQ ID NO: 3
 Genbank Entry
 Type: UNA
 Organism: HUMAN
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RESULT 3
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 Sequence: 16890 Application US/09864761
 Patent No.: US20020048761A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENE/EXON DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Aomic-X-1
 CURRENT FILING DATE: 2001-05-23
 PRIOR AFFILIATION NUMBER: US 60/180,312
 PRIOR AFFILIATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,365
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/246,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30





Liu, G., MacLean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Melarini, J., Meneus, I., Mihov, T., Mlengwa, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, P., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Petta, F., Rise, C., Rytov, P., Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Romann, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, B., Viel, R., Vo, A., Wilson, R., Wu, X., Wyman, D., Young, G., Zaidoun, J., Zemek, L., Zimmer, A. and Zody, M.

TITLE JOURNAL

Submitted (06-Aug-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Oct 27, 2001 this sequence version replaced j1.16355513.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WBIR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L838

Center clone name: 81_A_22

----- Summary Statistics

Sequencing vector: M13; M77815; 40% of reads

Sequencing vector: Plasmid; n/a; 60% of reads

Chemistry: Dye-primer-amersham; 2% of reads

Chemistry: Dye-terminator Big Dye; 98% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 168221 bases at least Q40

Consensus quality: 175650 bases at least Q30

Consensus quality: 178768 bases at least Q20

Insert size: 203600; agarose-1p

Insert size: 181495; sum-of-contigs

Quality coverage: 7.6 in Q20 bases.

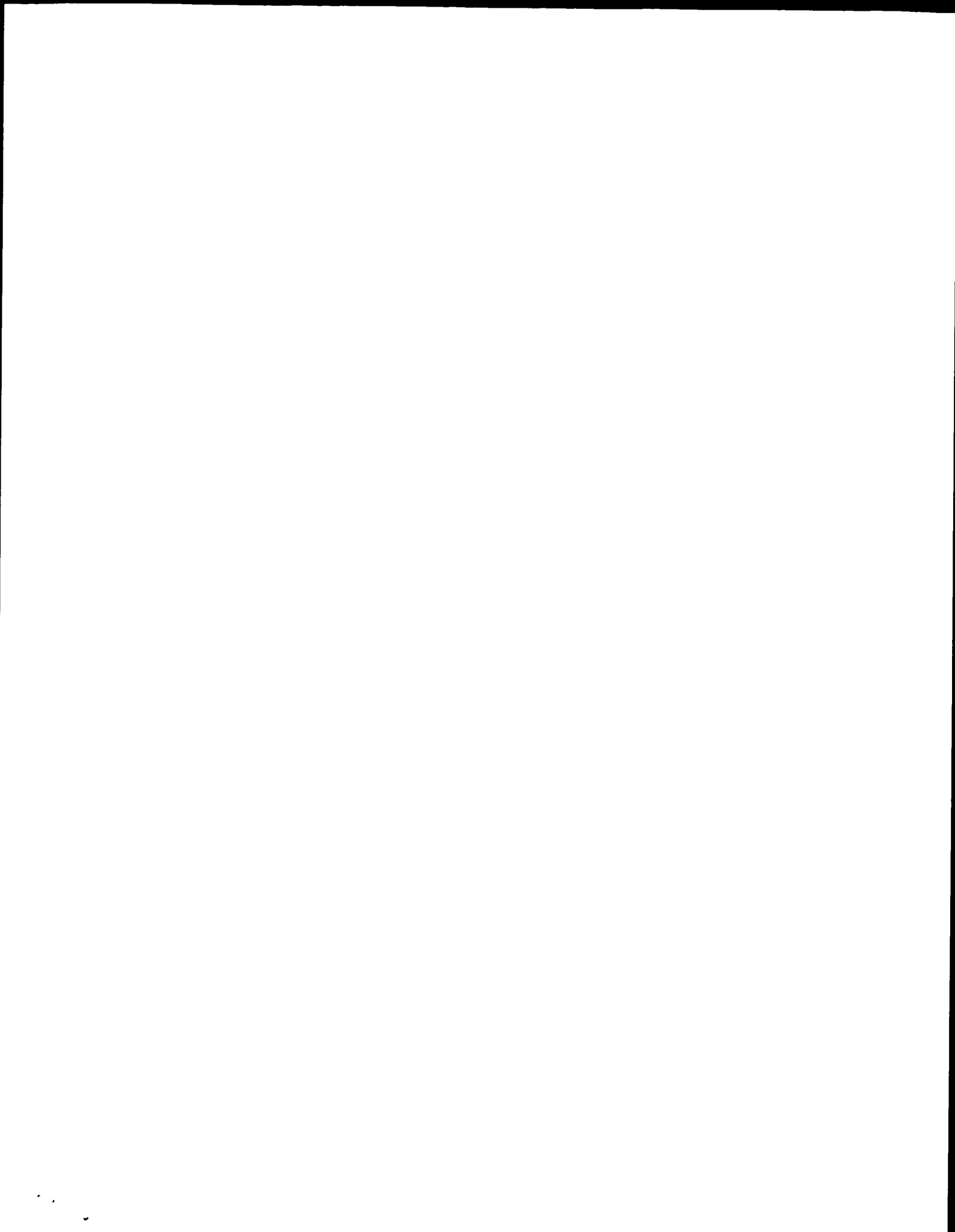
* NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

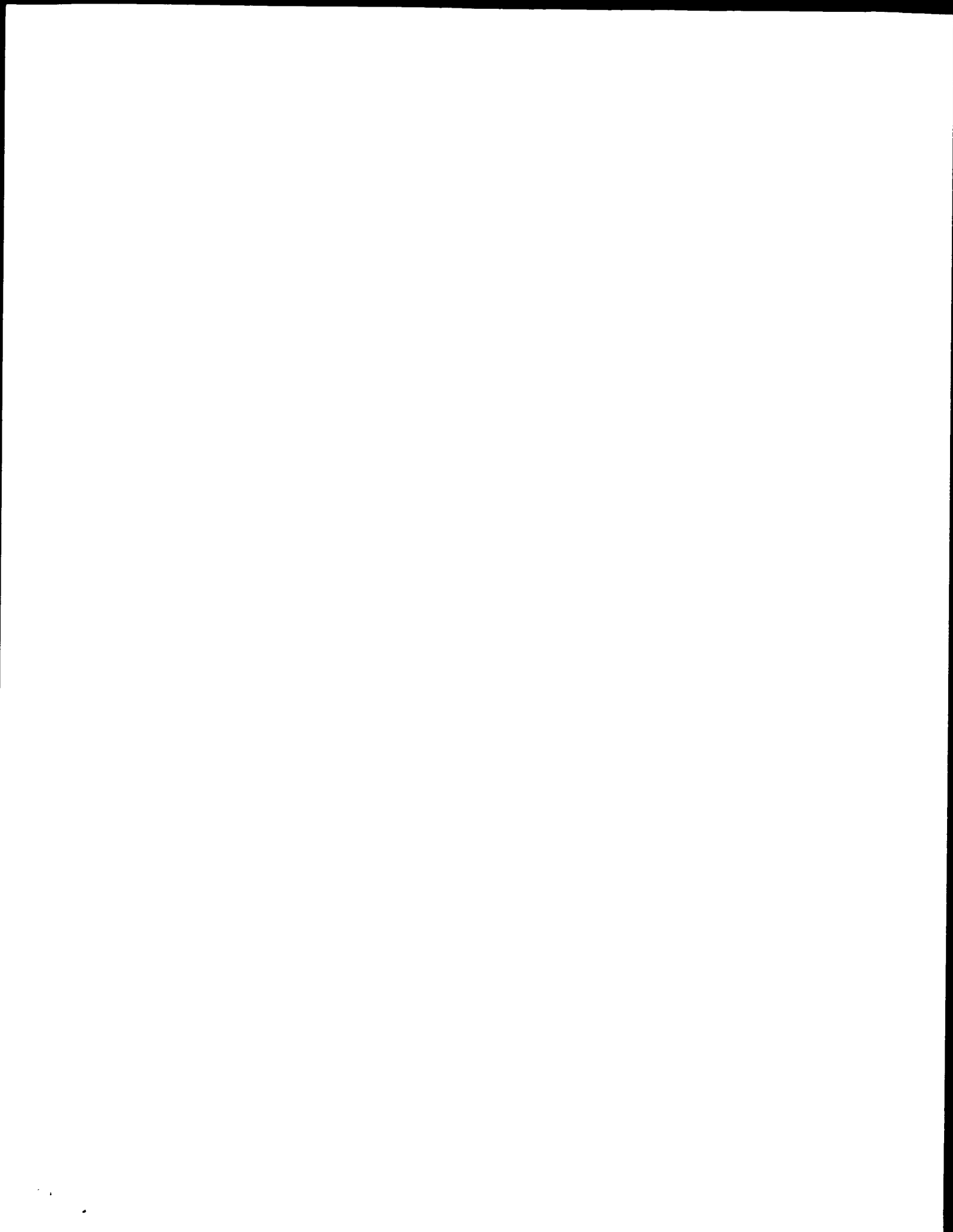
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* 10664 10763: gap of 100 bp
* 10764 11392: contig of 629 bp in length
* 11393 11492: gap of 100 bp
* 11493 12333: contig of 841 bp in length
* 12334 12433: gap of 100 bp
* 12434 13332: contig of 899 bp in length
* 13333 13432: gap of 100 bp
* 13433 14716: contig of 1284 bp in length
* 14717 14816: gap of 100 bp
* 14817 16101: contig of 1285 bp in length
* 16102 16201: gap of 100 bp
* 16202 17797: contig of 1596 bp in length
* 17798 17897: gap of 100 bp
* 17898 18949: contig of 1052 bp in length
* 18950 19049: gap of 100 bp
* 19050 20494: contig of 1445 bp in length
* 20495 20594: gap of 100 bp
* 20595 21775: contig of 1181 bp in length
* 21776 21875: gap of 100 bp
* 21876 23459: contig of 1584 bp in length
* 23460 23559: gap of 100 bp
* 23560 25831: contig of 2272 bp in length
* 25832 25931: gap of 100 bp
* 25932 27763: contig of 1832 bp in length
* 27764 27863: gap of 100 bp
* 27864 29986: contig of 2123 bp in length
* 29987 30086: gap of 100 bp

* 30087 32675: contig of 2589 bp in length
* 32676 32775: gap of 100 bp
* 32776 46266: contig of 3491 bp in length
* 36267 36366: gap of 100 bp
* 36367 39687: contig of 3321 bp in length
* 39688 39787: gap of 100 bp
* 39788 42811: contig of 3024 bp in length
* 42812 42911: gap of 100 bp
* 42912 47748: contig of 4837 bp in length
* 47749 47848: gap of 100 bp
* 47849 52056: contig of 4208 bp in length
* 52057 52156: gap of 100 bp
* 52157 56257: contig of 4101 bp in length
* 56258 56357: gap of 100 bp
* 56358 62535: contig of 6178 bp in length
* 62536 62635: gap of 100 bp
* 62636 65138: contig of 2503 bp in length
* 65139 65238: gap of 100 bp
* 65239 65640: contig of 4402 bp in length
* 69641 69740: gap of 100 bp
* 69741 74838: contig of 5098 bp in length
* 74839 74938: gap of 100 bp
* 74939 79482: contig of 4544 bp in length
* 79483 79582: gap of 100 bp
* 79583 81888: contig of 2306 bp in length
* 81889 81988: gap of 100 bp
* 81989 89859: contig of 7871 bp in length
* 89860 89959: gap of 100 bp
* 89960 158380: contig of 68421 bp in length
* 158381 158480: gap of 100 bp
* 158481 156923: contig of 8443 bp in length
* 166924 167923: gap of 100 bp
* 167924 176904: contig of 9881 bp in length
* 176905 177004: gap of 100 bp
* 177005 184595: contig of 7591 bp in length.

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/db_xref="taxon:9606"
/map="17"
/clone_lib="RMT-11 Human Male BA"
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/note="assembly_fragment"
clone_end:Sp6
vector_side:left
10764..11392
/note="assembly_fragment"
11493..12333
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12434..13332
/note="assembly_fragment"
13433..14716
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14817..16101
/note="assembly_fragment"
16202..17797
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17898..18949
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19050..20494
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21876..23459
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Pred. No.:	5,39c-106	6,12
Score:	1046.00	203
Percent Similarity:	100.00%	c
Local Similarity:	100.00%	c
Query Match:	99.05%	c
DB:	22	c
	Gaps:	
	Underls:	
	Prismal ches:	
	Conserved inva:	
	Matches:	
	Length:	

US-09-727-770-2 (1-205) x ABA46570 (1-612)

RESULTS

ABA64433
 100% ABA64433 standard: INA: 612 bp.

XX
XX

01-FEB-2002 (first entry)

XX
of Human foetal liver single exon nucleic acid probe #12738.

XX *... nucleic acid probe; ss.*

(5) *Homo sapiens*.

XX 11-667510000M

XX XX

04-FEB-2000; 2000US-0180412.
26-JUN-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
6-AUG-2000; 2000US-0632466.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236459.
04-OCT-2000; 2000US-0024264.
(MOLE) MOLECULAR DYNAMICS INC.
Penn St., Hanzel 1K, Chen W., Rank LR;
WPI; 2001-483447/52.
Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human fetal liver.
Claim 4; SEQ ID NO 12738; 639pp + sequence listing; English.
The invention relates to a single exon nucleic acid probe for
measuring human gene expression in a sample derived from human fetal
liver. The single exon nucleic acid probes may be used for predicting
measuring and displaying gene expression in samples derived from human
fetal liver. The present sequence is a single exon nucleic acid
probe of the invention.
Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at http://wipo.int/pub/published_pat_sequences.
sequences 613 pp; 120 A; 195 C; 151 G; 146 T; 0 other;

Alignment Scores:	$n = 496$	106	612
Pred. No.:	1046	00	204
Score:	100.00%		
Percent Similarity:	100.00%		
Best Local Similarity:	100.00%		
Query Match:	99.05%		
DB:	22		
		Matches:	Length:
		Conservative:	0
		Matches:	0
		Indels:	0
		Gaps:	0

nc-09-727-770-2 (1-205) x ABΛ6,4433 (1-612)

QY	1	MetSerAspAsnSerProCysIleValAlaLeuValPheThrIleSerGlyAlaMetAlaThr	210
DB	3	ATGTCCAAACAAAGCCCGAGATGCTTTGGTTTTCATCTCTGGATGGTATGGTGGAT	62
QY	21	MetValSerSerGlyLeuGlyAlaAlaCysGlyMetAlaCysAspGlyThrGlyIleMet	40
DB	63	ATGGCTCTCACTAGTCAGCTGGTGGTCTGGCTTGGCTAAGCTCAAGCAATGCAATG	122
QY	41	AlaMetSerValMetTrpProGlnGluTetHisMetLysSerIleIleProValValMet	60
DB	123	GCATGTCTCTGCATGTAGGCTAGAGCTCATCTCAATCAAGATATATATATATGGTATG	192
QY	61	AlaGlyIleIleThrIleCysGlyLeuValAlaValProIleAlaAsnSerLeuAsn	81
DB	183	GTCTGGTATCATCACTATCATGGTATGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTG	242
QY	81	AspAspAsnSerLeuTrpSerSerPheLeuGlnLeuGlyAlaCysSerGlyLeuAla	100
DB	244	CATCACAAACATCTCTATATAGTATCTCTCTAGCTGGATCAAGCTGGTGGTGGTA	302
QY	101	AlaCysPheAlaIleValIleValGlyAspThrGlyLysCysGlyThrAlaGlnIlePro	120
DB	303	GGCCGGCTTGGCCATGGCTCATCTGGGGGCACTGGCTGGCACTGGTACAGAGG	362
QY	121	ArgLeuPheValGlyMetIleLeuIleLeuIlePheAlaIleValLeuIleLeuSerThr	140
DB	363	CGACTATTGTAGGCATGATATCATATGCTATATCTTCTCAAGGGGTCTATCTCTCA	422
QY	141	LysIleProLeuSerLysProThrSerHisAlaIleAlaCysLysAspHisProSerSer	160
DB	423	AAGTAGCCGCTCTCAAAACCAACCACTCATCTCAACAAATACATCTAAAGCACTCA	482

Tue Dec 31 14:03:15 2002

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PR 40-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DK;
XX WPI; 2001-488900/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO: 12982; 65bp + Sequence listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
XX
XX Sequence 612 BP; 120 A; 195 C; 151 G; 146 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 5,496-106 Length: 612
XX Score: 1046.00 Matches: 203
XX Percent Similarity: 100.00% Conservat: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 99.05% Indels: 0
XX DB: 22 Gaps: 0
XX
XX
XX US-09-727-770-2 (1-205) x AAK48619 (1-612)
XX
XX
XX 1 MetSerAsnSerProGlyValAlaLeuValPheThrIleSerGlyAlaMetAlaThr 20
XX
XX 3 AAGTCAACACAGCCGAGATGCTTGGATTTCACCATCTCGGAGCTATGGCCACC 62
XX
XX 21 MetValSerSerGlyLeuGlyAlaGlyGlyLeuGlyAlaGlyAsnGlyThrGlyIleMet 40
XX
XX 63 ATGGTCTCAGTGGCTGGTGTCTGTCTGTGCAATAGCAAAATGGCAAGGAGATCAAG 122
XX
XX 41 AlaMetSerValMetTppProGlnLeuIleHisMetLysSerIleGluProValValMet 60
XX
XX 123 GCATGCTGTGATCTGGAGAGCTGAGAGCTGAGTACAGCAAGATCTGATGATGATGATG 182
XX
XX 61 AlaGlyIleIleThrIleTyrGlyLeuValAlaAlaValProProAlaAsnSerLeuAsn 80
XX
XX 183 GTGGTATATCAACCATATCATGCGGATAGTGGAGGCTGGTGGGCTGGCAACCTGCAAT 242
XX
XX 81 AspAspAsnSerLeuTyrSerSerPheLeuIleLeuValAlaLeuValLeuSerGlyLeuAla 100
XX
XX 243 GATGACCAACAGTCTCTATAGCATTTCTCTCAGCTGGAGGAGTGGATGAGTGGATGGCA 302
XX
XX 101 AlaGlyPheAlaIleValIleValGlyAspThrGlyLysCysGlyThrAlaGlnGlnPro 120
XX
XX 303 GCGGCTTTGCCATCTGATCTGGAGGACATGATGATGATGATGATGATGATGATGATGATG 362
XX
XX 121 ArgLeuPheValGlyMetIleLeuIleLeuIlePheAlaGlyValLeuIleLeuSerThr 140
XX
XX 463 CGACATATTTGTAGGATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 422
XX
XX 141 LysGlnProLeuSerLysProThrSerHisArgTlleA:AcGlySerAspIleProSerSer 160
XX
XX 423 AAGACGCTCTCTCAAAACCCACATCATGACAGAAATACATGATGATGATGATGATGATGAT 482
XX
XX 161 PheArgAsnLysGlnProAspThrHisValLeuGlySerTppProSerValValAspLeu 180
XX
XX 483 TTGGAGGAACAAACAGAGCTGACAGCAATGTCGAGGAGTGGTGGTGGTGGTGGTGGTGGT 542

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QY 181 LeuSerValGlnCysProGlyValHisArgLeuValPheThrIleSerGlyAlaMetAlaThr 200
XX
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XX
XX 201 HisAlaVal 203
XX
XX 603 CATGCTGCTG 611
XX
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XX ID AAK48619 standard; DNA; 612 BP.
XX
XX AAK48619;
XX
XX 06-NEW 2001 (first entry)
XX
XX Human bone marrow expressed single exon probe SEQ ID NO: 13176.
XX
XX DE
XX KW human; bone marrow expressed exon; gene expression analysis; probes;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX OS Homo sapiens.
XX
XX PN W0230157276-A2.
XX
XX 09-AUG-2001.
XX
XX 40-JAN-2001; 2001WO-0500668.
XX
XX 04-FEB-2000; 2000US-0180412.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
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XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DK;
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow
XX
XX Example 4; SEQ ID NO: 13176; 65bp + Sequence listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX the probes of the invention.
XX
XX Sequence 612 BP; 120 A; 195 C; 151 G; 146 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 5,496-106 Length: 612
XX Score: 1046.00 Matches: 203
XX Percent Similarity: 100.00% Conservat: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 99.05% Indels: 0
XX DB: 22 Gaps: 0
XX
XX
XX US-09-727-770-2 (1-205) x AAK48619 (1-612)
XX
XX
XX 1 MetSerAsnSerProGlyValAlaLeuValPheThrIleSerGlyAlaMetAlaThr 20
XX
XX 3 AAGTCAACACAGCCGAGATGCTTGGATTTCACCATCTCGGAGCTATGGCCACC 62
XX
XX 21 MetValSerSerGlyLeuGlyAlaGlyGlyLeuGlyAlaGlyAsnGlyThrGlyIleMet 40
XX
XX 63 ATGGTCTCAGTGGCTGGTGTCTGTCTGTGCAATAGCAAAATGGCAAGGAGATCAAG 122
XX
XX 41 AlaMetSerValMetTppProGlnLeuIleHisMetLysSerIleGluProValValMet 60
XX
XX 123 GCATGCTGTGATCTGGAGAGCTGAGAGCTGAGTACAGCAAGATCTGATGATGATGATG 182
XX
XX 61 AlaGlyIleIleThrIleTyrGlyLeuValAlaAlaValProProAlaAsnSerLeuAsn 80
XX
XX 183 GTGGTATATCAACCATATCATGCGGATAGTGGAGGCTGGTGGGCTGGCAACCTGCAAT 242
XX
XX 81 AspAspAsnSerLeuTyrSerSerPheLeuIleLeuValAlaLeuValLeuSerGlyLeuAla 100
XX
XX 243 GATGACCAACAGTCTCTATAGCATTTCTCTCAGCTGGAGGAGTGGATGAGTGGATGGCA 302
XX
XX 101 AlaGlyPheAlaIleValIleValGlyAspThrGlyLysCysGlyThrAlaGlnGlnPro 120
XX
XX 303 GCGGCTTTGCCATCTGATCTGGAGGACATGATGATGATGATGATGATGATGATGATGATG 362
XX
XX 121 ArgLeuPheValGlyMetIleLeuIleLeuIlePheAlaGlyValLeuIleLeuSerThr 140
XX
XX 463 CGACATATTTGTAGGATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 422
XX
XX 141 LysGlnProLeuSerLysProThrSerHisArgTlleA:AcGlySerAspIleProSerSer 160
XX
XX 423 AAGACGCTCTCTCAAAACCCACATCATGACAGAAATACATGATGATGATGATGATGATGAT 482
XX
XX 161 PheArgAsnLysGlnProAspThrHisValLeuGlySerTppProSerValValAspLeu 180
XX
XX 483 TTGGAGGAACAAACAGAGCTGACAGCAATGTCGAGGAGTGGTGGTGGTGGTGGTGGTGGT 542

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us-09-727-770-2.p2n.rng

Tue Dec 31 14:03:15 2002

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AA144608
ID AA144608 standard; DNA: 612 bp.
XX
AC AA144608;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #14294 used to measure gene expression in human placenta sample.
XX
KW Probe: microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN W3200157272-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US000663.
XX
PR 04 FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0612466.
PR 21-SEP-2000; 2000US-0244687.
PR 27-SEP-2000; 2000US-0246359.
PR 04-OCT-2000; 2000GB-0024263.
XX
(MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DK;
XX
WF1: 2001-48897/53.
XX
DE Human genome-derived single exon nucleic acid probes useful for
DE analyzing gene expression in human placenta.
XX
PS Claim 25; SEQ ID NO 13294; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 612 BP; 120 A; 195 C; 151 G; 146 T; 0 other;

Alignment Scores:
Pred. H3.: 5,390-106 Length: 612
Score: 1046.00 Matches: 209
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.05% Indels: 0
Gaps: 0
DB:

US-09-727-770-2 (1-205) x AA144608 (1-612)
QY 1 MetSerAsnSerProGluTyrAlaLeuValPheThrIleSerGlyAlaMetAlaThr 20
DB 3 ATGTC/AACCAACAGCCGACGATATAGCTTTGCGTTTCACCAATCTCGGTCATGGCCAGC 62
QY 21 MetValSerThrGlyLeuGluAlaValSerGlyMetAlaValSerGlyThrIleMet 40
DB 63 ATGGTCTCAGTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 122
QY 41 AlaMetSerValMetTrpProGluLeuIleIleMetLysSerIleIleProValValMet 60
DB 123 GCGATCTCTCTCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 182
QY 61 MetGlyIleThrIleThrIleThrIleThrIleThrIleThrIleThrIleThrIle 80
DB 183 GCTGGTATCATCAGCAATCATGAGCTAGTGGCTAGTGGCTAGTGGCTAGTGGCTAGTGGCT 242

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Tue Dec 31 14:03:15 2002

CC and hyaline membrane disease. The present sequence is a single exon probe open reading frame of this invention.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from Wipo at

CC http://wipo.int/patdb/patdbseq_f_3_en.jsp

XX
SQ Sequence 612 BP; 120 A; 195 C; 151 G; 146 T; 0 other;

Alignment Scores:
Pred. No.: 5,396-106 Length: 612
Score: 1046.00 Matches: 203
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.95% Indels: 0
DB: 24 Gaps: 0

US-09-727-770-2 (1-205) x AB012486 (1-612)

QY 1 MetSerAsnSerProGluTyrAlaLeuValPheThrIleSerGlyAlaMetAlaThr 20
Db 3 ATCTCAACACAGGCGGAGATATATTTGGCTTTTCACCATCTGCGTCTAATGCGCACC 62
QY 21 MetValSerSerGlyLeuGlyAlaAlaPheGlyMetAlaIleAspGlyThrGlyIleMet 40
Db 63 AUGTCTCCAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 122
QY 41 AlaMetSerValMetTrpProGluLeuIleIleHisMetLysSerIleIleProValValMet 60
Db 123 GCATGTCGTGATGTCGACAGAGCTGATGTCACATGACATGATCCATCATCCAGTGGTCATG 182
QY 61 AlaGlyIleIleThrIleThrGlyLeuValAlaAlaValProProAlaAsnSerLeuAsn 80
Db 183 GCTGGTATCAACACATCTATGCGCTAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
QY 81 AspAspAsnSerLeuTyrSerSerPheLeuGlyIleGlyAlaGlyLeuSerGlyIleAla 100
Db 243 GATGCAACACATCTATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
QY 101 AlaGlyPheAlaIleValIleValGlyAspThrGlyIleGlySerGlyThrAlaGluGlnPro 120
Db 403 GTCGACTTTGCTGATGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 362
QY 121 AraLeuPheValGlyMetGlyIleLeuIleLeuIlePheAlaIleValLeuIleLeuSerThr 140
Db 363 GCATATTGTAGGATGATACATCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
QY 141 LysGlnProLeuSerLysProThrSerHisAlaIleAlaGlySerGlySerSerSerSer 160
Db 424 AAGCAGCGCTCTGCAAAACCGACAGTCACAGATACATGATGATGATGATGATGATGATGAT 482
QY 161 PheAlaGlyAspLysGlnProAspThrHisValIleGlySerTrpProSerValValAspLeu 180
Db 483 TTCTGGACAAACACACCTGACACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
QY 181 LeuSerValGlnCysProAlaValHisArgLeuLeuAlaAlaProCysProLeuProPro 200
Db 543 CTAAGTGTACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
QY 201 HisAlaVal 204
Db 603 CATGCTGTG 611
RESULT 12
ID ABA99210 standard; DNA: 1160 BP.
XX ABA99210;
AC ABA99210;
XX 29-JUL-2002 (first entry)
DE Human tumour specific antihaemic peptide encoding sequence #2.
XX

KW Proton pump inhibitor; tumour specific antihaemic peptide;
cytostatic; tumour; ds; human.

XX Homo sapiens.

XX Location/Qualifiers

FI 229..696

FT /ftaq: a

FT /product: "tumour specific antihaemic peptide"

XX JP2001286284 A.

XX 16-OCT-2001.

XX 05-APR-2000; 2000JP-0103966.

XX 05-APR-2000; 2000JP-0103966.

XX (SABU) SATO N.

XX (SABU) SATO N.

XX (YAMA) YAMAGUCHI M.

XX WPI: 2002-134186/18.

XX P-PSDB: ABB08456.

XX Gene diagnostic agent and gene treating agent for tumours comprises

XX using tumour-specific antigen and proton pump inhibitor as antitumor

XX agent.

XX claim 9; Page 49-40; 80pp; Japanese.

XX This invention relates to a diagnostic agent or treating agent for

XX tumours by using a tumour specific antigen and a proton pump

XX inhibitor. The method is cytostatic in its action and the

XX tumour-specific antigen peptide is useful for treating and preventing

XX cancers. This nucleotide sequence is a human tumour-specific

XX antihaemic peptide-encoding sequence.

XX Sequence 1160 BP; 175 A; 429 C; 412 G; 253 T; 0 other;

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[illegible][illegible]

El treatment and diagnosis of cancer, immune disorders, cardiovascular
 disorders and neurological diseases

XX Title 1: Page 533; 1299pp; English.

XX Sequences AAF21614 - AAF22041 represent cDNA sequences encoding human
 proteins AAF58711 - AAF59124. The cDNA and protein sequences are
 associated with breast and ovarian cancer. Included in the invention are
 sequences AAF22042 - AAF22049 and AAF59125 which are used in the
 isolation and characterization of the DNA and protein sequences of the
 invention. The breast and ovarian cancer associated DNA, protein, antigen
 or antiserum sequences exhibit cytostatic, immunosuppressive,
 neurotropic, neuroprotective, antiviral, antiallergic, hepatotropic,
 antidiabetic, antiinflammatory, antitumor, antineurotic, anticonvulsant,
 antibacterial, antifungal, antiparasitic and cardiac activity. The
 polypeptide and protein sequences are used in the diagnosis of cancer,
 particularly breast and ovarian cancer. The nucleic acid sequences,
 proteins, antisera and antisense may also be used in the diagnosis,
 prevention and treatment of immune disorders e.g. Addison's disease,
 diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 arthritis and ulcerative colitis; cardiovascular disorders such as
 myocardial ischaemia; wound healing; neurological diseases such as
 cerebral anoxia and epilepsy; and infectious diseases.

XX Sequence 1150 BP; 224 A; 369 C; 288 G; 256 T; 11 other;

Alignment Scores:

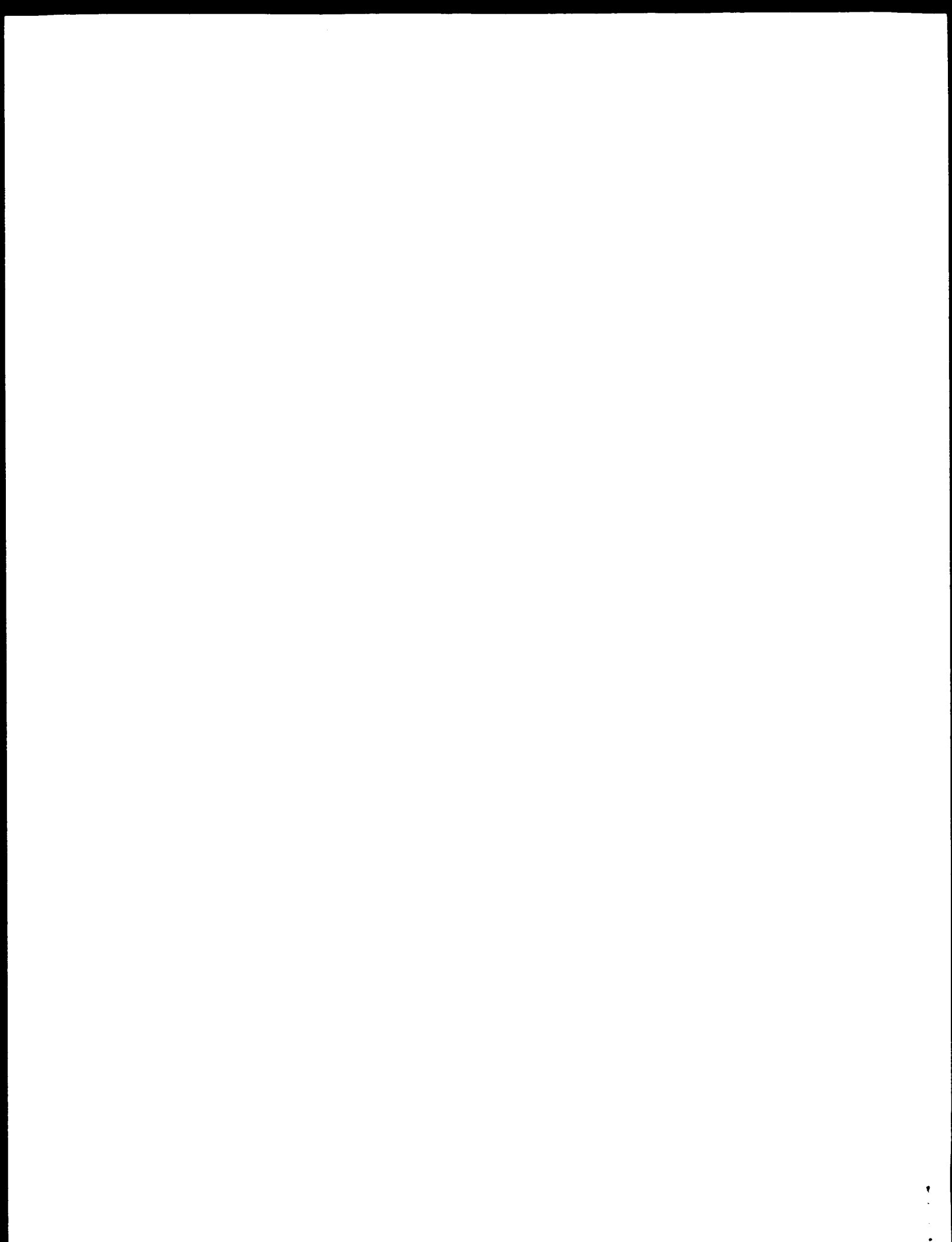
Prod. No.:	Score:	Length:	Matches:
1	4,750.00	1150	146
2	625.00	146	146
3	71.23%	10	10
4	66.67%	43	43
5	59.19%	21	21
6	21	4	4

US-09-727-770-2 (1-205) x AAF21682 (1-1150)

QY	6	ProGlyTyrAlaLeuValPheThrIleSerGlyAlaMetAlaIleThrMetValSerSer---	24
DB	143	CCAAAGCTACCTCGGAGCTCTAGTATCTAACTGGGCTCTGTCTGAGCTGCTACCC	202
QY	25	-----GlyLeuGlyAlaAlaCysGlyMetAlaIleAsuGlyThrGlyIle	39
DB	203	CGCTTCCTCCACAGCTGGGCGGTGGGCTATGGTAAGGTAACAGGCTACGACCT	262
QY	40	MetAlaMetSerValMetIrrProGluLeuIleHisMetLysSerIleIleProValVal	59
DB	263	GAGAGCATGTCTGTCATGAGGAGGAGAGATC---ATGAGCTCATCATCTGCTGCTG	419
QY	60	MetAlaGlyIleIleThrIleIleTyrlglyLeuValAlaAlaValProProAlaAsuSerIleu	79
DB	320	ATGGTGGGATCATGCTATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	479
QY	80	AsuAspAsuSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer	95
DB	380	AATGAGCATCATGCTCTATACAGAGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT	439
QY	90	IleuSerGlyIleAlaAlaGlyPheAlaIleValIleValIleValIleValIleValIle	115
DB	440	CTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	499
QY	116	ThrAlaGlnGlnAlaGlnPheValGlyMetIleLeuIleLeuIleLeuIleLeuIleVal	145
DB	500	ACGAGACAGACGAGGAGATATGCTGGGCTATGCTGCTGCTGCTGCTGCTGCTGCTG	559
QY	146	-----LeuIleLeuSerThrLysGlnProLeuSerLys	146
DB	560	CTGGGCTCTACGCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	619
QY	147	ProThrSerHisAlaIleAlaGlyCysAspHisProSerSerPheArgAsuLysGlnPro	166
DB	620	CTGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	679

QY	167	AspThrHisValLeuGlySerIrrProSerValValAspLeuLeuSerValGlnCysPro	186
DB	680	GACACATACGACGGGCGGCTGG-CCGCTAGTCTGTTGACATGCGACGTGCTCT	738
QY	187	ArgValHisArgLeuLeuAlaArgProCysProLeuProProHisAlaValAspIle	205
DB	739	ATGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	795

Search completed: December 28, 2002, 11:02:56
 Job time : 261 secs




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1 PRIOR APPLICATION NUMBER: US 60/237,456
2 PRIOR FILING DATE: 2000-05-26
3 PRIOR APPLICATION NUMBER: US 09/762,466
4 PRIOR FILING DATE: 2000-08-03
5 PRIOR APPLICATION NUMBER: GR 24263.6
6 PRIOR FILING DATE: 2000-10-04
7 PRIOR APPLICATION NUMBER: US 60/236,454
8 PRIOR FILING DATE: 2000-05-27
9 PRIOR APPLICATION NUMBER: PCT/US01/00666
10 PRIOR FILING DATE: 2001-01-30
11 PRIOR APPLICATION NUMBER: PCT/US01/00667
12 PRIOR FILING DATE: 2001-01-30
13 PRIOR APPLICATION NUMBER: PCT/US01/00664
14 PRIOR FILING DATE: 2001-01-30
15 PRIOR APPLICATION NUMBER: PCT/US01/00669
16 PRIOR FILING DATE: 2001-01-30
17 PRIOR APPLICATION NUMBER: PCT/US01/00665
18 PRIOR FILING DATE: 2001-01-30
19 PRIOR APPLICATION NUMBER: PCT/US01/00668
20 PRIOR FILING DATE: 2001-01-30
21 PRIOR APPLICATION NUMBER: PCT/US01/00663
22 PRIOR FILING DATE: 2001-01-30
23 PRIOR APPLICATION NUMBER: PCT/US01/00662
24 PRIOR FILING DATE: 2001-01-30
25 PRIOR APPLICATION NUMBER: PCT/US01/00661
26 PRIOR FILING DATE: 2001-01-30
27 PRIOR APPLICATION NUMBER: PCT/US01/00670
28 PRIOR FILING DATE: 2001-01-30
29 PRIOR APPLICATION NUMBER: US 60/234,687
30 PRIOR FILING DATE: 2000-04-21
31 PRIOR APPLICATION NUMBER: US 09/608,408
32 PRIOR FILING DATE: 2000-06-30
33 PRIOR APPLICATION NUMBER: US 09/714,203
34 PRIOR FILING DATE: 2001-01-24
35 NUMBER OF SEQ ID NOS: 49117
36 SOFTWARE: Annonmax Sequence Listing Engine
37 SEQ ID NO 16890
38 LENGTH: 612
39 TYPE: DNA
40 ORGANISM: Homo sapiens
41 FEATURE:
42 OTHER INFORMATION: MAP TO A:305473.2
43 OTHER INFORMATION: EXPRESSED IN BT474, S
44 OTHER INFORMATION: EXPRESSED IN HELA, S
45 OTHER INFORMATION: EXPRESSED IN PLACENTA
46 OTHER INFORMATION: EXPRESSED IN BONE MAR
47 OTHER INFORMATION: EXPRESSED IN FETAL LI
48 OTHER INFORMATION: EXPRESSED IN LUNG, S
49 OTHER INFORMATION: EXPRESSED IN ADULT LI
50 OTHER INFORMATION: EXPRESSED IN BEAN, S
51 OTHER INFORMATION: EXPRESSED IN HUMAN, S
52 OTHER INFORMATION: EXPRESSED IN H100, S
53 OTHER INFORMATION: EST H17: g1450243, INV
54 OTHER INFORMATION: EST HUMAN HIT: B57269
55 OTHER INFORMATION: SWISSPROT HIT: P23967
56 (S: 04-864-763-16890

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Db 325 TCCTGCTGATGCTATTCGAAATGCTGGTGATGCTGGTGCTTAGACGGAATGCGCAACAA 384
QY 120 ProArdelePheValGlyMetIleleuIleleuIleleuIleleuIleleuIleleu 138
DB 385 CCGAAGCTGTTTGTGGGAATCATCTGATCTCTATCTTTGGCGAAGCGCTTGCACATG 441

RESULT 8
US-09-770-149-323
: Sequence 323, Application US/09770149
: Patent No. US20020059663A1
: GENERAL INFORMATION:
: APPLICANT: Gorlach, Jörn
: APPLICANT: An, Yong-Qiang
: APPLICANT: Hamilton, Carol M.
: APPLICANT: Price, Jennifer L.
: APPLICANT: Raines, Tracy M.
: APPLICANT: Yu, Yang
: APPLICANT: Ramezani, Joshua G.
: APPLICANT: Page, Amy
: APPLICANT: Matthew, Abraham V.
: APPLICANT: Ledford, Brooke L.
: APPLICANT: Wessner, Jeffrey P.
: APPLICANT: Haas, William David
: APPLICANT: Garcia, Carlos A.
: APPLICANT: Krickler, Maja
: APPLICANT: Slader, Ted
: APPLICANT: Davis, Keith P.
: APPLICANT: Allen, Keith
: APPLICANT: Hoffman, Neil
: APPLICANT: Burban, Patrick
: TITLE OF INVENTION: Expressed Sequences of Arabidopsis
: FILE REFERENCE: 2024 (PARA-01399V)
: CURRENT APPLICATION NUMBER: US/09770149
: CURRENT FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/178,506
: PRIOR FILING DATE: 2000-01-27
: NUMBER OF SEQ ID NOS: 999
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 323
: LENGTH: 686
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-770-149-323

Alignment Scores:
Pred. No.: 2,296-26 Length: 686
Score: 308.00 Matches: 73
Percent Similarity: 64.03% Conservatives: 16
Best Local Similarity: 52.52% Mismatches: 42
Query Match: 29.17% Indels: 8
Gaps: 2
DB:

US-09-727-770-2 (1-205) x US-09-770-149-323 (1-686)
QY 7 GluTyraAlaLeuValPheThrIleSerGlyAlaMetAlaThrMetValSerSerglyLeu 26
DB 45 GAAATGCTGCTTCTTCCTTCGATTCCTTGGCGGCGCGCGCTGCTGCTTCTTCCTGATG 104
QY 27 GlyAlaAlaCysGlyMetAlaTyrAsnGlyIleMetAlaMetSerValMetTrp 46
DB 105 GGAGAGCGGTACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 164
QY 47 ProGluLeuIleHisMetLysSerIleIleProValValMetAlaGlyIleIleThrIle 66
DB 165 CAGAGCTTGCG---ATGAATCGATGTCCTTCTTATGCTGAGCTGAGTTAGGTATT 221
QY 67 TyroGlyLeuValAlaValProProAlaAsnSerLeuAsnAspAsnSerLeuTyr 86
DB 232 TAGCTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 281
QY 87 SerSerPhe-----LeuGlnLeuGlyAlaGlyLeuSerglyLeu 99
DB 111

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Db 282 TATCTATTGATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
QY 100 AlaAlaGlyPheAlaIleValIleValGlyAspIleGlyLysGlyIleAlaIleLeu 119
DB 342 TCCGCCGCTATGCTATTCGAAATGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 401
QY 120 ProArdelePheValGlyMetIleleuIleleuIleleuIleleuIleleuIleleu 138
DB 402 CCAAGTTGTTTGGGAGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 408

RESULT 9
US-09-887-576-815
: Sequence 815, Application US/09887576
: Patent No. US20020344047A1
: GENERAL INFORMATION:
: APPLICANT: Hudworth, P.
: APPLICANT: Brown, D.
: APPLICANT: Chapp, H.
: APPLICANT: Zhu, T.
: APPLICANT: Bao, H.
: APPLICANT: Wang, X.
: APPLICANT: Cooper, Bret
: TITLE OF INVENTION: Promoters for regulation of plant expression
: FILE REFERENCE: 1360.001US1
: CURRENT APPLICATION NUMBER: US/09887576
: CURRENT FILING DATE: 2001-06-25
: PRIOR APPLICATION NUMBER: US 69/214,848
: PRIOR FILING DATE: 2003-06-24
: PRIOR APPLICATION NUMBER: US 60/214,087
: PRIOR FILING DATE: 2000-06-24
: PRIOR APPLICATION NUMBER: US 69/258,692
: PRIOR FILING DATE: 2000-12-29
: NUMBER OF SEQ ID NOS: 875
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 815
: LENGTH: 498
: TYPE: DNA
: ORGANISM: Oryza sativa
US-09-887-576-815

Alignment Scores:
Pred. No.: 1,886-26 Length: 498
Score: 407.00 Matches: 74
Percent Similarity: 64.03% Conservatives: 16
Best Local Similarity: 52.52% Mismatches: 42
Query Match: 29.07% Indels: 8
Gaps: 2
DB:

US-09-727-770-2 (1-205) x US-09-887-576-815 (1-498)
QY 7 GluTyraAlaLeuValPheThrIleSerGlyAlaMetAlaThrMetValSerSerglyLeu 26
DB 25 GAGACGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 84
QY 27 GlyAlaAlaCysGlyMetAlaTyrAsnGlyIleMetAlaMetSerValMetTrp 46
DB 85 GGGGGCGGCTACGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 144
QY 47 ProGluLeuIleHisMetLysSerIleIleProValValMetAlaGlyIleIleThrIle 66
DB 145 CCGGAGCTGCTG---ATGAATCGATGTCCTTCTTATGCTGAGCTGAGTTAGGTATT 201
QY 67 TyroGlyLeuValAlaValProProAlaAsnSerLeuAsnAspAsnSerLeuTyr 86
DB 202 TAGCGCTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261
QY 87 SerSerPhe-----LeuGlnLeuGlyAlaGlyLeuSerglyLeu 99
DB 262 TAGCTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
QY 100 AlaAlaGlyPheAlaIleValIleValGlyAspIleGlyLysGlyIleAlaIleLeu 119
DB 322 CCTGCGGAGATGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481

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QY 120 ProArdeupheValGlyMetIleLeuIleLeuIleLeuIleLeuIleLeu 138
DB 382 CCAAGACGCTGGTGGTATGATGATGATGATGATGATGATGATGATGATG 438

RESULT 13
US-09-887-576-775
: Sequence 775, Application US/09887576
: Patent No. US20020144047A1
: GENERAL INFORMATION:
: APPLICANT: Budworth, P.
: APPLICANT: Brown, D.
: APPLICANT: Chang, H.
: APPLICANT: Zhu, T.
: APPLICANT: Han, B.
: APPLICANT: Wang, X.
: APPLICANT: Cooper, Bret
: TITLE OF INVENTION: Promoters for regulation of plant expression
: FILE REFERENCE: 1360.001US1
: CURRENT APPLICATION NUMBER: US 60/297,878
: PRIOR FILING DATE: 2001-06-23
: PRIOR APPLICATION NUMBER: US 60/213,848
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: US 60/214,087
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: US 60/258,692
: NUMBER OF SEQ ID NOS: 875
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 775
: LENGTH: 500
: TYPE: DNA
: ORGANISM: Oryza sativa
US-09-887-576-775

Alignment Scores
Prod. No.: 1,896-26 Length: 500
Score: 307.00 Matches: 73
Percent Similarity: 64.00% Gaps: 14
Best Local Similarity: 52.52% Mismatches: 42
Query Match: 26.07% Indels: 6
DB: 10 Gaps: 2

US-09-727-770-2 (1-205) x US-09-887-576-775 (1-500)

QY 7 GlyAlaLeuValPheThrIleSerGlyAlaMetAlaThrMetValSerSordGlyLeu 26
DB 25 GAGACGGCCCTTCTTCGCTGCTTCGGCGCGGGTTCGGCTGCTATCTGCTGCGATG 87
QY 27 GlyAlaAlaCysGlyMetAlaLysAsnGlyThrGlyIleMetAlaMetSerValMetTrp 46
DB 86 GAGCGGAGCTAGCGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 147
QY 47 ProGluLeuIleHisMetLysSerIleIleProValValMetAlaGlyIleIleThrIle 66
DB 148 ATGGAGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 204
QY 67 TyrGlyLeuValAlaAlaValProAlaAlaSerIleAsuAspAspAsuSerLeuIle 86
DB 205 TACGGATTCATCAATGCGGATTCATCAATGCGGATTCATCAATGCGGATTCATCAATG 264
QY 87 SerSerPhe----- LeuGluLeuGlyAlaGlyLeuSerGlyLeu 99
DB 265 TTGCTTTGAGAGGTTAGCGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
QY 100 AlaAlaGlyPheAlaIleValIleValGlyAspThrGlyLysCysGlyThrAlaGlnGln 119
DB 325 GCGCGGCGCATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATG 484
QY 120 ProArdeupheValGlyMetIleLeuIleLeuIleLeuIleLeuIleLeu 138
DB 385 CCAAGACGCTGGTGGTATGATGATGATGATGATGATGATGATGATGATG 441

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RESULT 11
US-09-887-576-814
: Sequence 814, Application US/09887576
: Patent No. US20020144047A1
: GENERAL INFORMATION:
: APPLICANT: Budworth, P.
: APPLICANT: Brown, D.
: APPLICANT: Chang, H.
: APPLICANT: Zhu, T.
: APPLICANT: Han, B.
: APPLICANT: Wang, X.
: APPLICANT: Cooper, Bret
: TITLE OF INVENTION: Promoters for regulation of plant expression
: FILE REFERENCE: 1360.001US1
: CURRENT APPLICATION NUMBER: US 60/298,692
: PRIOR FILING DATE: 2001-06-25
: PRIOR APPLICATION NUMBER: US 60/213,848
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: US 60/214,087
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: US 60/258,692
: NUMBER OF SEQ ID NOS: 875
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 814
: LENGTH: 498
: TYPE: DNA
: ORGANISM: Oryza sativa
US-09-887-576-814

Alignment Scores
Prod. No.: 2,450-26 Length: 498
Score: 356.20 Matches: 72
Percent Similarity: 64.04% Conservative: 17
Best Local Similarity: 51.80% Mismatches: 42
Query Match: 28.98% Indels: 8
DB: 10 Gaps: 2

US 29 727 770 2 (1-205) x US 29 887 576 814 (1-498)

QY 7 GlyAlaLeuValPheThrIleSerGlyAlaMetAlaThrMetValSerSordGlyLeu 26
DB 25 GAGACGGCCCTTCTTCGCTGCTTCGGCGCGGGTTCGGCTGCTATCTGCTGCGATG 84
QY 27 GlyAlaAlaCysGlyMetAlaLysAsnGlyThrGlyIleMetAlaMetSerValMetTrp 46
DB 85 GAGCGGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 144
QY 47 ProGluLeuIleHisMetLysSerIleIleProValValMetAlaGlyIleIleThrIle 66
DB 145 GCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201
QY 67 TyrGlyLeuValAlaAlaValProAlaAlaSerIleAsuAspAspAsuSerLeuIle 86
DB 202 TACGGCTTCATCAATGCGGATTCATCAATGCGGATTCATCAATGCGGATTCATCAATG 261
QY 87 SerSerPhe----- LeuGluLeuGlyAlaGlyLeuSerGlyLeu 99
DB 262 TACCTCTTTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTC 421
QY 100 AlaAlaGlyPheAlaIleValIleValGlyAspThrGlyLysCysGlyThrAlaGlnGln 119
DB 422 GTTGGAGGAATGCTATGCGGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 381
QY 120 ProArdeupheValGlyMetIleLeuIleLeuIleLeuIleLeuIleLeu 138
DB 482 CCAAGACGCTGGTGGTATGATGATGATGATGATGATGATGATGATGATG 438

RESULT 12
US-09-887-576-778
: Sequence 778, Application US/09887576
: Patent No. US20020144047A1
: GENERAL INFORMATION:

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```

; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US 09/887,576
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 778
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-887-576-778

```

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Alignment Scores:
Pred. No.: 1,590-25 Length: 510
Score: 299.00 Matches: 74
Percent Similarity: 63.12% Conservat: 15
Best Local Similarity: 52.48% Mismatches: 42
Query Match: 28.31% Indels: 10
Gaps: 3
DB:

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US-09-727 770-2 (1-205) x US-09-887-576-778 (1-510)

```

QY 7 GluTyrAlaLeuValPheThrIleSerGlyAlaMetAlaThrMetValSerGlyLeu 26
DB 31 GAGAGGGGGGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCT 90
QY 27 GlyAlaAlaGlySerGlyMetAlaAlaGlySerGlyMetAlaAlaGlySerGlyMet 46
DB 91 GGGGGGGGGGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCT 150
QY 47 ProLeuLeuIleHisMetLeuSerGlyMetAlaAlaGlySerGlyMetAlaAlaGly 66
DB 151 GGGGGGGGGGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCT 207
QY 57 TyrGlyLeuValAlaAlaValProProAlaAsnSerLeuAsnAspAspAsnSerLeu 86
DB 208 TACGGGCTCATCATGGGCTCATCATGGGCTCATCATGGGCTCATCATGGGCTCATCAT 267
QY 87 SerSerPhe 99
DB 268 TCCCTCTTCGAGGCTACGGGCTACGGGCTACGGGCTACGGGCTACGGGCTACGGGCT 327
QY 100 AlaAlaGlyPheAlaAlaValIleValGlyAspThrLeuSerGlyThrAlaGln 119
DB 328 GCGGGGGGGGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCT 387
QY 120 ProArgLeuPheValGlyMet 137
DB 388 CCAAAACGTTTGTGGGTATGATCTATCTATCTATCTATCTATCTATCTATCTATCT 447
QY 148 Leu 138
DB 448 CTC 450

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RESULT 14
US-09-887-576-786
; Sequence 786, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.

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; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US 09/887,576
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 786
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-887-576-786

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Alignment Scores:
Pred. No.: 4,640-24 Length: 543
Score: 286.50 Matches: 78
Percent Similarity: 57.40% Conservat: 19
Best Local Similarity: 46.15% Mismatches: 51
Query Match: 27.13% Indels: 21
Gaps: 4
DB:

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US-09-727-770-2 (1-205) x US-09-887-576-786 (1-543)

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QY 4 AsnSerProGluTyrAlaLeuValPheThrIleSerGlyAlaMetAlaThrMetValSer 24
DB 16 AACGGAGAGAGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGG 75
QY 24 SerGlyLeuGlyAlaAlaGlySerGlyMetAlaGlySerGlyMetAlaGlySerGly 43
DB 76 TCATGATCGAGGGGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGGGCTTGGGG 145
QY 44 ValMetTrpProGluLeuIleHisMetAlaSerIleIleProValValMetAlaGly 63
DB 136 GAGAGGGGGGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCT 192
QY 64 IleThrIleTyrGlyLeuValAlaAlaValProProAlaAsnSerLeuAsnAspAsn 83
DB 193 CTGGGGCTCATCATGGGCTCATCATGGGCTCATCATGGGCTCATCATGGGCTCATCAT 252
QY 84 SerLeuTyrSerSerPhe 96
DB 253 ATGGGCTCATCATGGGCTCATCATGGGCTCATCATGGGCTCATCATGGGCTCATCAT 412
QY 97 SerGlyLeuAlaAlaGlyPheAlaIleValIleValGlyAspThr GlyLysCysGly 116
DB 313 TCGGGGGGGGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCT 472
QY 116 ValAlaGlnProArgLeuPheValGlyMetIleLeuIleLeuIlePheAlaValIle 146
DB 373 CGGGGAGGAGGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCTTCTTCTGAGCT 442
QY 136 4
DB 433 TGGGGCTCATCATGGGCTCATCATGGGCTCATCATGGGCTCATCATGGGCTCATCAT 492
QY 147 roThrSer-----HisArgIle 152
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RESULT 14
US-09-887-576-466
; Sequence 466, Application US/09887576

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Db	1465	ATACGCAAAATTTGTGTTTGATGACAGCGCAATTCACACAGCAAGCTTTTCGTTGG	1424
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Db	1425	TATGATCTATGCTCATTTTCAGTGCAGAGCTTCTGCTA	1464

Search completed: December 29, 2002, 12:21:56
Job time : 60 secs

GenCore version 5.1.4
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 28, 2002, 10:26:51 : Search time 2:57.5 seconds
(without alignments)
233,922 hits, 11,156,111 updates/sec

File: us-09-727-770-2

Perfect score: 1056

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Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Ugapop 6.0 , Ugapext 7.0

Igapop 6.0 , Igapext 7.0

Searched: 2054640 seqs, 14551402978 residues

Total number of hits satisfying chosen parameters: 4107280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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26: qb.ba*

27: qb.ba*

28: qb.ba*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1056	100.0	633	6	AX337957 Sequence
2	1056	100.0	633	6	AX337959 Sequence
3	1056	100.0	151999	2	AF005473 Homo sapi
4	1056	100.0	104595	2	AF015414 Homo sapi
5	1043	98.8	139384	2	AC109333 Homo sapi
6	673	63.7	1078	9	BC007759 Homo sapi
7	673	63.7	1086	9	BC004537 Homo sapi
8	673	63.7	1123	9	BC005290 Homo sapi
9	673	63.7	1143	9	BC007389 Homo sapi
10	626.5	59.3	1162	9	BC008187 Homo sapi
11	616	58.3	1975	9	BC010147 Homo sapi
12	604	57.3	1153	10	MUSMUS
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20	524.5	49.7	110303	9	BC0192M17
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ALIGNMENTS

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us-09-727-770-2.p2n.rge

Tue Dec 31 14:03:15 2002

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DEFINITION Sequence 1 from Patent WO/0194380.
ACCESSION AX337957
VERSION AX337957.1 GI:18128674
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Li, Z., Wei, M., Ketchum, K., and Heasley, E.M.
TITLE Isolated human transporter proteins, nucleic acid molecules
encoding human transporter proteins, and uses thereof
JOURNAL Patent: WO 0194380-A 1 14-DEC-2001;
Applera Corporation Robert A. Millman Assistant Secretary (US)
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Location/Qualifiers
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Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 6 Gaps: 0
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QY 61 AlaGlyIleIleThrIleThrIleThrIleThrIleThrIleThrIleThrIleThr 80
DB 190 GCTGCTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 249
QY 81 AspAspAsnSerLeuValSerPheLeuGlnIleGlyAlaGlyLeuSerGlyLeuAla 100
DB 250 GATGACAAACAGCTCTATAGCAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 309
QY 101 AlaGlyPheAlaIleValIleValIleValIleValIleValIleValIleValIle 120
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QY 121 ArgLeuPheValGlyMetIleLeuIleLeuIlePheAlaLysValIleLeuSerThr 140
DB 370 CGACATATTCTAGGCAAGATCATCTCATCTCATCTCTCTCTCTCTCTCTCTCTCT 429
QY 141 LysGlnProLeuSerLysProThrSerHisSarqIleCysLysAspHisProSerSer 160
DB 430 AAGCAGCGGCTCTCAAAACCCAGCAGTATGCTGCTGCTGCTGCTGCTGCTGCTG 489
QY 161 PheArqAsnLysGlnProAspThrHisValLeuGlyLysTrpProSerValIleAspLeu 180
DB 490 TTCCGGAACAAACAGCTCTCAAAACCCAGCAGTATGCTGCTGCTGCTGCTGCTG 549
QY 181 LeuSerValIleGlnCysProArqValHisSarqIleCysLysAspHisProSerSer 200
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 QY 22 ValSerSerGlytGlyAlaAlaGlySerLeuAlaAlaGlySerLeuAlaAla 41
 DB 185 GCTTTCAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 244
 QY 42 MetSerValMetTrrpProGluLeuHisMetLysSerLeuProValMetAla 61
 DB 245 ATGCTCTCATCGCGCGCGGAGAGATC---ATGAATGCCATTATCCCGAGTGTGCT 301
 QY 62 GlytLeuLeuThrLeuGlyCysLeuValAlaAlaValProProAlaAsnSerLeuAsp 81
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 QY 82 AspAsnSerLeuTyrSerSerPheLeuLeuLeuLeuAlaAlaAlaAlaAla 97
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 QY 118 GluInProAlaLeuPheValGlyMetLeuLeuLeuLeuLeuLeuLeuLeu 135
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 QY 136 -----LeuLeuLeuSerThrGlySerProLeuSerLysProThr 148
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 QY 149 SerHisArgGlyArgCysLysAspHisProSerSerPheArgAsnLysGlnProAspThr 168
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 REFERENCE 1 (bases 1 to 1086)
 AUTHORS Strausberg, R
 TITLE Direct Submission

JOURNAL

REMARK
COMMENT

NIH MGC Project URL: <http://mdc.nci.nih.gov>
 Contact: MGC help desk
 Email: mgc-help@nci.nih.gov
 Tissue Procurement: ATCC/ATCC/DIP
 cDNA Library Preparation: Rabin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LBNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Gaithersburg, Maryland
 Web URL: <http://www.ncbi.nlm.nih.gov>
 Contact: nisc-mgc@nci.nih.gov
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 Benjamin, B., Hakesley, W.W., Koutler, G.S., Kirkley, J., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S., Lee, H., Leppas, R.,
 Lim, M., Maduro, Q., Masferrer, J., Mustian, S.D., Moskay, J.,
 Salazar, L., Sengupta, K., Shender, B., Stancovski, S., Thomas, P.,
 Truong, R., Touchman, J.W., Tsunquian, C., Voth, J., Walker, M.A.,
 Zhang, L.H., and Green, E.D.

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 This clone was selected for full length sequencing because it
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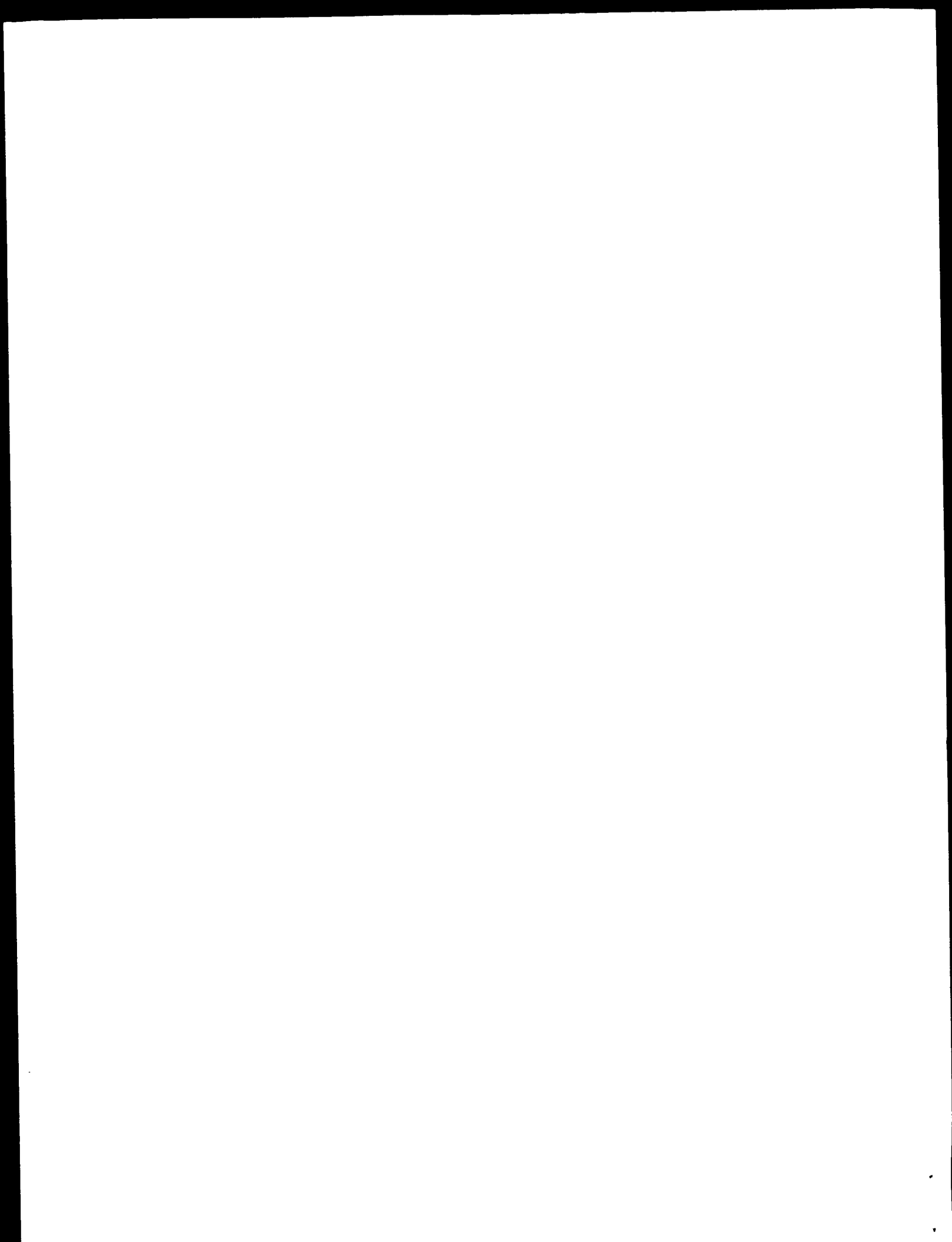
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ORIGIN

Alignment Scores:
 Pred. No.: 2,770-51 Length: 1086
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 Best Local Similarity: 70.05% Mismatches: 42
 Query Match: 63.73% Indels: 15
 DB: 9 Gaps: 3
 US-09-727-770-2 (1-205) x BC004547 (1-1086)

QY 2 SerAsuAsnSerProGlytAlaValPheThrHisSerGlyAlaMetAlaThrMet 21
 DB 137 ICCAAGACGGCGCGGAGTATGCTTTCTTCGGCGATGCGCGCGCGGCGGATG 196
 QY 22 ValSerSerGlytGlyAlaAlaGlySerLeuAlaAlaGlySerLeuAlaAla 41
 DB 197 GCTTTCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 256
 QY 42 MetSerValMetTrrpProGluLeuHisMetLysSerLeuProValMetAla 61
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 QY 62 GlytLeuLeuThrLeuGlyCysLeuValAlaAlaValProProAlaAsnSerLeuAsp 81

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201		

Job time : 2657 secs



[illegible]

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RESULTS 3
US-09-864-761-16890
Sequence ID#99, Application #9, US99-4761
Patent No. US2002004876(A1)
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GERM-LINE-DERIVED SINGLE EXON NUCLEOTIDE ACID PROBES
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: 93-60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 6,672,077,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,466
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: 04-24263,6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: 05-60/2346,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/006666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/JP01/006667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/006662
PRIORITY FILING DATE: 2001-01-30

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RESULT 2
US-09-727-770-3
> Seq. Accession: R54113.1; US-09727770
> Patent No. US20020147305A1
> GENERAL INFORMATION:
> APPLICANT: WEI, Ming-Hui
> APPLICANT: WEI, Ming-Hui
> APPLICANT: KETCHUM, Karen A.
> APPLICANT: KEASLEY, Ellen M.
> TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS
> TITLE OF INVENTION: ROLIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
> TITLE OF INVENTION: AND USES THEREOF
> FILE REFERENCE: C1000651
> CURRENT APPLICATION NUMBER: US-09-727-776
> CURRENT FILING DATE: 2000-12-04
> PRIOR APPLICATION NUMBER: US-60/208,836
> PRIOR FILING DATE: 2000-06-02
> NUMBER OF SEQ ID NOS: 3
> SOFTWARE: FASTSEQ for Windows Version 4.0
> SEQ ID NO 3
> LENGTH: 6339
> TYPE: DNA
> ORGANISM: HUMAN
US-09-727-770-3

Query Match          98.9%; Score 626; DB 10; Length 6339;
Best Local Similarity 100.0%; Prod No 8 40-177;
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8  ACAGTGCACCAACAGAGCCCGAGATATGCTTTGCTTTTCACATCTGAGGGTATGAGCCA 67
1b      2498  ACACTGCACACAGAGCCCGAGATATGCTTTGCTTTTCACATCTGAGGGTATGAGCCA 3057

QY      68  GCACGCTGCTCGARTGGCTGAGGTGTGCTCTGTGCGATGGGCAACAGATGCAACGGCATCA 127
1b      3058  ACATGCTTCAGTGGGCTGAGGTGTGCTCTGTGCGATGGGCAACAGATGCAACGGCATCA 3117

QY      128  TCCGATATCTGTGATGTGGCCACAGTGCATTCACATGAAGTCCATCATCCAGTGTCA 187
1b      3118  TGGGCTATCTGTGATGTGGCCACAGTGCATTCACATGAAGTCCATCATCCAGTGTCA 3177

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Computer I.D.

M protein nucleotide search, using frame_plus_p2n model

Run on: December 28, 2002, 10:56:01 : Search time 1974 seconds
(without alignments)
1681.902 Million cell updates/sec

Title: US-09-727-770-2
Perfect score: 1056
Sequence: 1 MSNRPYALVFHISAMAT.....PQVRLARVLIIPHAVDI 205

Scoring Table: BLOSUM62
Xgapop 10.0 : Xgapext 0.5
Ygapop 10.0 : Ygapext 0.5
Fgapop 6.0 : Fgapext 7.0
Delop 6.0 : Deloxt 7.0

Searched: 1615466 seqs, 807714770 residues

Total number of hits satisfying chosen parameters: 4266432

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus_p2n_model -DEV-xlib
-Q=us09-727-770-2.p2n.rst -MINMATCH=61 -FAP=10 -LAPEXT=0
-DB=EST -QFMT=lastgap -SUFFIX=p2n.rst -MINMATCH=61 -FAP=10 -LAPEXT=0
-UNITS=bits -STAPT=1 -FAP=1 -MATPIX=blosum62 -SPANS human40.cdi -LIST=45
-DOALIGN=200 -THE_SCOPE=ptl -THE_MAX=100 -THP_MIN=0 -ALIGN=15 -MCDE=LOCAL
-OUTFMT=ptl -NORM=ext -HPAPITS=500 -MENIPN=0 -MAXIPN=2000000000
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-WARN_LTIMEOUT=10 -THREADS=1 -XAPAP=10 -XAPEXT=0.5 -FAPAP=0.5 -FAPEXT=7
-YGAP=10 -YGAPEXT 0.5 -DELAP 6 -DELEXT=7

Database :

EST :
1: em_estha :
2: em_esthum :
3: em_esthum :
4: em_esthum :
5: em_esthum :
6: em_estpl :
7: em_estpl :
8: em_estpl :
9: ob_est1 :
10: ob_est2 :
11: ob_est3 :
12: ob_est3 :
13: ob_est4 :
14: ob_est5 :
15: em_esthum :
16: em_esthum :
17: ob_est1 :
18: em_gss_hum :
19: em_gss_hum :
20: em_gss_hum :
21: em_gss_vrt :
22: em_gss_hum :
23: em_gss_hum :
24: em_gss_hum :
25: em_gss_hum :
26: em_gss_hum :
27: em_gss_hum :

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	674.5	63.9	1061	13	BM562656	BM562656 AGNCOURT
2	673	63.7	908	14	BQ722145	BQ722145 AGNCOURT
3	673	63.7	981	14	BQ676034	BQ676034 AGNCOURT
4	673	63.7	993	14	BM463421	BM463421 AGNCOURT
5	673	63.7	1063	14	BQ653546	BQ653546 AGNCOURT
6	673	63.7	1081	14	BQ232887	BQ232887 AGNCOURT
7	668	63.3	996	14	BQ058594	BQ058594 AGNCOURT
8	666	63.1	986	14	BQ232102	BQ232102 AGNCOURT
9	666	63.1	923	14	BQ424541	BQ424541 AGNCOURT
10	664	62.9	1076	14	BQ229405	BQ229405 AGNCOURT
11	664	62.9	1201	13	BM473665	BM473665 AGNCOURT
12	662	62.7	991	14	BM918349	BM918349 AGNCOURT
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16	659	62.4	1222	13	BM478359	BM478359 AGNCOURT
17	654	61.9	872	14	BQ722238	BQ722238 AGNCOURT
18	654	61.8	696	14	BM791194	BM791194 K-EST0071
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21	648	61.4	634	14	BM843350	BM843350 K-EST0121
22	648	61.4	638	14	BM818948	BM818948 K-EST0086
23	648	61.4	657	14	BM769872	BM769872 K-EST0053
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ALIGNMENTS

RESULT 1
LOCUS BM562656 1061 bp mRNA linear EST 20-FEB-2002
DEFINITION AGNCOURT_6566751 NIH_MGC_H8 Homo sapiens cDNA clone IMAGE:5736584
5', mRNA sequence.
ACCESSION BM562656
VERSION BM562656.1 GI:18808930
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1061)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)


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QY 22 ValSerSerCLeuGlyAlaAlaGlySerMetAlaAlaGlySerMetAlaAlaGlySerMetAlaAla 41
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QY 42 MetSerValMetTrpProGluGluGluHisMetLysSerGluHisLeuValValMetAla 61
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QY 62 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 81
DB 205 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 264
QY 82 AspAsnSerLeuTyrSerSerThrLeuLeuLeuLeuValAla-----GlyLeuSer 97
DB 265 GACATCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 324
QY 98 GlyLeuAlaAlaGlyPheAlaLeuValLeuValGlyAspThrLeuLysGlyThrAla 117
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QY 118 GlnGlnProArgGluPheValGlyMetThrLeuLeuLeuLeuLeuPheAlaAlaVal----- 135
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QY 149 SerHisArgLysCysLysAspHisProSerSerPheAlaAsnLysGlnProAspThr 168
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QY 169 HisValLeuGlySerTrpProValValAspLeuLeuSerValGlnLysProArgVal 188
DB 565 TACGACAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 623
QY 189 HisArgLeuLeuAlaArgProCysProGluProSerProSerValValAspThr 205
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AGENCOREL2034321 NIH_MGC_112 Homo sapiens cDNA 5' end IMAGE:5585806
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KEYWORDS EST.
SOURCE Human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 981)
AUTHORS NIH MGC http://mgi.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Published (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rqs@nsl.nih.gov
Tissue procurement: NIH/DIP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI)
DNA Sequenced by: Amersham Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNI at:
http://image.llni.gov
Plates: L10M2380 rows: 6 columns: 93
High quality sequence stop: 709.
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1..981
Features: "mimo syngens"
"chr xxx" "image:5585806"
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/lab_host "DH10R (phage-resistant)"
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GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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Prod. No.: 673.00 Matches: 152
Score: 70.19% Conservative: 9
Best local similarity: 70.05% Mismatches: 42
Query Match: 63.74% Indels: 15
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QY 22 ValSerSerCLeuGlyAlaAlaGlySerMetAlaLysAspThrGlyIleMetAla 41
DB 158 GCTTCAGGCGCTGGAGGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 217
QY 42 MetSerValMetTrpProGluLeuLeuLeuLeuMetLysSerIleLeuProValValMetAla 61
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QY 62 GlyIleIleThrLeuGlyLeuValAlaAlaValProProAlaAsnSerLeuAsnAsp 91
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DB 335 GACATCAGGCTCAGCAGAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 394
QY 98 GlyLeuAlaAlaGlyPheAlaLeuValLeuValGlyAspThrLeuLysGlyThrAla 117
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QY 118 GlnGlnProArgGluPheValGlyMetThrLeuLeuLeuLeuLeuPheAlaAlaVal----- 135
DB 455 CAGCAGCCCGGAGTATGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 514
QY 136 -----LeuLeuLeuSerThrLysGlnProLeuSerLysProThr 148
DB 515 GCTACGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574
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DB 575 AGCACAAGAAATATTATGTAAGACACACACACACACACACACACACACACACACACACACACAC 634
QY 169 HisValLeuGlySerTrpProSerValValAspLeuLeuSerValGlnLysProArgVal 188
DB 635 TACGACAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 693
QY 189 HisArgLeuLeuAlaArgProCysProGluProSerProSerValValAspThr 205
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RESULTS
BQ678034 BQ678034 981 bp mRNA Human Liver EST 05 FEB 2002
AGENCOREL2034321 NIH_MGC_112 Homo sapiens cDNA 5' end IMAGE:5585806
5' mRNA sequence.
ACCESSION BQ678034

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Tue Dec 31 14:03:17 2002

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VERSION      RM464421.1  GI:18512463
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SOURCE       human.
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             Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE    1 (bases 1 to 993)
AUTHORS      NIH MGC http://www.ncbi.nlm.nih.gov/
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: rstrauss@mail.nih.gov
             Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM2352 row: k column: 23
             High quality sequence: 711.
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             /db_xref="taxon:9606"
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             full-length clones and constructed by Life Technologies.
             Note: this is a NIH_MGC Library."
BASE COUNT  159 a 369 c 259 g 206 t
ORIGIN
Alignment Scores:
Pred. No.: 993
Score: 673.00
Percent Similarity: 74.19%
Best Local Similarity: 70.05%
Query Match: 63.73%
Indels: 15
Gaps: 3
DB:
US-09-727-770-2 (1-295) x RM464421 (1-993)
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Db 101 TCCAGAGAGGGGGCGGAGTATGCTTGGTTTCGGGTCATGGGGGCGGCGGCGCATG 160
QY 22 ValSerSerGlyLeuGlyAlaAlaGlyGlyGlyMet*AlaLeuAsnGlyGlyGlyLeuMetAla 41
   ||| ||| ||||| ||||| ||| ||||| ||||| ||| ||||| ||||| |||
Db 161 GTCTTCAGGCGCTCGGGGCTGGCTATGGACAGGCAAGAGAGAGTACGGGCAATCGGGGCG 220
QY 42 MetSerValMetTrpProGluLeuIleIleMetLeuSerIleIleProValValMetAla 61
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Db 221 ATGCTGCTCAAGCGGGGCGGAGAGATC---ATGAAGTCCATCATCATCCAGTCCGTCACAGCT 277
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Db 278 GGCATCATCGGCATCTACGGGCTGGTGGTGGGAGTCTCATGCTCAACTGGCTGAATGAG 337
QY 82 AspAsnSerLeuLeuIleValGlyLeuValGlyLeuValGlyLeuValGlyLeuValGlyLeu 97
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Db 438 GACATCAGCGCTCTACAGAGAGTTCGTCAGCTCGAGGCGGCGGCTGAGCGTGGCGCTGAGC 397
QY 98 GlyLeuAlaAlaGlyPheAlaIleValIleValGlyAspThrGlyGlyGlyGlyGlyTrpAla 117
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QY 118 GlnGlnProAcLeuPheValGlyMetIleLeuIleLeuIlePheAlaLysVal----- 135
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Db 458 CAGCAGCGCGGACATATTCGTCGGGAGCATGATGATCTCATCTTCATCTTTCGACAGCTCTGAG 517
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Db 518 CTTACAGCTCTCACTCGCGGCTCATCTTCCTCAAAATAGACAGCTCTCGAGCTTACG 577
QY 149 SerHisArgIleArgCysLysAspHisProSerSerPheAlaAsnLysGlnProAspThr 168
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Db 578 AGCCACAGAAATATATGTAACACACAGCTCTCTCATTTTCAACAGCAACACATTCACAA 637
QY 169 HisValLeuGlySerTrpProSerValValAspLeuLeuSerValGlnCysProArgVal 188
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Db 638 TAGCAGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 696
QY 189 HisArgLeuLeuAlaArgProCysProLeuLeuProHisAlaValAspIle 205
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Db 697 CATCGCTCTCTTCGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 747
RESULT 5
RM053546 1063 bp mRNA linear EST 25 MAR 2002
AGENCOUNT_6845437 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:594542
5', mRNA sequence.
ACCESSION   RM053546
VERSION     RM053546.1 GI:19812886
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE    1 (bases 1 to 1063)
AUTHORS      NIH MGC http://www.ncbi.nlm.nih.gov/
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: rstrauss@mail.nih.gov
             Tissue Procurement: Dr. Daniel McVicar, DRS/NCI
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM2122 row: a column: 23
             High quality sequence: 692.
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             /clone_1ib="NIH_MGC_106"
             /class="type="natural killer cells, cell line"
             /note="Jordan; blood; Vector: pGEMT; Site_1: XbaI; Site_2:
             EcoRI; cDNA made by oligo dT priming, directionally cloned
             into EcoRI/XbaI sites using the following 5' adaptor:
             GACGACGAC(G). Library constructed by Lind Bond in the
             laboratory of Gerald M. Rubin (University of California,
             Berkeley) using ZAP cDNA synthesis kit (Stratagene) and
             Superscript II RT (Life Technologies). Note: this is a
             NIH_MGC Library."
BASE COUNT  176 a 370 c 401 g 215 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1063
Score: 673.00
Percent Similarity: 74.19%
Best Local Similarity: 70.05%
Query Match: 63.73%
Indels: 15
Gaps: 3
DB:
US 09 727 770 2 (1 295) x RM053546 (1-1063)

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ACCESSION: BQ279185
VERSION: BQ279185.1
KEYWORDS: EST, mRNA
SOURCE: Homo sapiens
ORGANISM: Homo sapiens
REFERENCE: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS: NIH-MGC
TITLE: National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL: Unpublished (1999)
COMMENT: Contact: Robert Strausberg, Ph.D.
Email: rstrauss@mail.nih.gov
Tissue Procurement: ATCC
cDNA library prepared by: The I.M.A.G.E. Consortium (LBNL)
DNA Sequencing by: Amersham Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LCM2045 row: m column: 17
High quality sequence stop: 710.

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Location/Qualifiers
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/clone_lib="NIH-MGC_107"
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/lab_host="pH10B (phage resistant)"
/note="Organ: breast; Vector: pOT7; Site: L; EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into pGEM2/3Xpl0 sites using the following 5' adaptor: GCCAGG(G). Library constructed by Ling Hong in the laboratory of Gerald E. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library."

BASE COUNT 150 a 348 c 247 q 193 t

ORIGIN
Alignment Scores:
Pred. No.: 3,876-62 Length: 928
Score: 660.00 Matches: 152
Percent Similarity: 73.85% Conservatives: 9
Best Local Similarity: 69.72% Mismatches: 42
Query Match: 62.50% Indels: 16
Gaps: 3

US-09-727-770-2 (1 205) x BQ279185 (1 929)
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QY 22 ValSerSerGlyLeuGlyAlaAlaGlyGlySerAlaAlaGlyAlaGlyThrGlyLeuAla 41
DB 158 GTCCTTCAGCGCGCTCGCGCGCTGATGCGACACCGCAAGCGGTACCGGGATTGCGGCC 217
QY 42 MetSerValMetTppProGluTyrTheHisMetLysSerTheHisProValValMetAla 61
DB 218 AUGTCTGTGTCATCGCGCGGAGACATC---ATGAAGTTCATCATGCCACTGCTATGCT 274
QY 62 GlyTtTheThrTheTyrGlyLeuValAlaAlaLProProValAlaAsnSorCuaAsp 81
DB 275 GGCATCATGCGCATCATACGCGCTGCGCGGACATGCGATGCGTAACTGCGTGAATGAC 334
QY 92 AspAsnSerLeuTyrSerSerSerTheLeuGluLeuGlyAla-----GluGluSer 97
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QY 98 GlyLeuAlaAlaGlyAlaLeuValTheValGlyAspThrGlyGlyGlyGlyGlyAla 117
DB 395 GGCCTGGCAGCGCGCTTGGCATCGGATATGCTGGGAGACGTGGAGTGGAGGACGAC 454
QY 118 GluInProArgLeuGlyMetLeuGluLeuLeuLeuLeuLeuLeuLeuLeuVal 135
DB 455 CAGTACGCGCGCACTATCTCGGCGATGATGATGATGATGATGATGATGATGATGATG 514
QY 136 -----LeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 148
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QY 149 SerHisArgIleArgCysIysAspHisSerSerSerSerSerSerSerSerSerSer 168
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QY 169 HisValLeuGlySerTppProSerValValAspLeuLeuSerValGluGlySerProAla 188
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QY 189 HisArgLeuLeuAlaArgProCysProLeuProProProHisAla ValAspThr 205
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RESULT 14
LOCUS: RM554691 1041 bp mRNA Linear EST 20 FEB 2002
DEFINITION: AGENCE00RL6545556 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5746924
5' mRNA sequence.
ACCESSION: RM554691 GI:18794503
VERSION: RM554691.1
KEYWORDS: EST.
SOURCE: human.
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE: 1 (bases 1 to 1041)
AUTHORS: NIH-MGC
TITLE: National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL: Unpublished (1999)
COMMENT: Contact: Robert Strausberg, Ph.D.
Email: rstrauss@mail.nih.gov
Tissue Procurement: ATCC
cDNA library prepared by: The I.M.A.G.E. Consortium (LBNL)
DNA Sequencing by: Amersham Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLM12746 row: d column: 13
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/lab_host="pH10B (phage-resistant)"
/note="Organ: Small Intestine; Vector: pGEM-Spout6; Site_1: Not 1; Site_2: Salt; cloned indirectly; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC library."

BASE COUNT 161 a 374 c 277 q 218 t 1 others

ORIGIN
Alignment Scores:
Pred. No.: 4,66-62 Length: 1041
Score: 660.00 Matches: 152
Percent Similarity: 73.85% Conservatives: 9
Best Local Similarity: 69.72% Mismatches: 42
Query Match: 62.50% Indels: 16

Db 741 CATGCTGTTCCTTCCCGGCTTATCCCCCGGCGCGCGCTGAC 782

Search completed: December 29, 2002, 12:19:27
Job time : 1978 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Computer Ltd.

em protein - nucleic search, using frame_plus_p2n model

run on: December 28, 2002 16:57:11 : search time 51 seconds
(without alignments)
1242.223 95.11 0.51 4.14 0.5/0.2

Title: US-09-727-770-2
Perfect score: 1056
Sequence: 1 MSNNSPEVALYETISGMAT.....PEVHLLAPPCHLPHAVCI 295

Scoring table: nuc-swm2

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 44162 scaps, 15318391 residues

Total number of hits satisfying chosen parameters: 982724

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH 0.1 -APP_query.fasta_1.391
-LIST-45 -DBALIGN=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS human40.cdi
-MODE=LOCAL -QFMT=ptc -NEMO-ext -HEAUS17P-500 -MINLEN=0 -MAXLEN=200000000
-USER=090972779-85CN 1.1.17 -result 27122002 394449.5870 -NOPS 6 -ICPU 3
-N-ALIGN 4 -XMAX 4 -ALIGN=0 -BLAST-442 -WA 1 -RBL 2 -MAX_LEN=0 130
-WAKN_TIME=0.40 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP 6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP 6 -DELEXT=7

Database: Issued_Patents_NA:

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2: 134.5 12.7 4982 4 US-09-229-059-1
3: 134.5 12.6 849 3 US-08-807-300-2
4: 100.5 9.5 697 1 US-08-254-494-2
5: 100.5 9.5 687 1 US-08-408-232B-2
6: 100.5 9.5 1120 1 US-08-408-222B-4
7: 96.5 9.1 1120 1 US-08-254-494-3
8: 89.5 8.5 3807 2 US-08-816-755-1
9: 89.5 8.5 3807 4 US-09-090-673-1
10: 84.5 8.0 31571 1 US-08-323-449B-1
11: 84.5 8.0 53526 4 US-08-658-146-2
12: 84.5 8.0 53577 4 US-08-658-146-1

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	100.5	9.5	687	1	US-08-408-232B-2 Sequence 2, Appl1
6	100.5	9.5	1120	1	US-08-408-222B-4 Sequence 3, Appl1
7	96.5	9.1	1120	1	US-08-254-494-3 Sequence 3, Appl1
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10	84.5	8.0	31571	1	US-08-323-449B-1 Sequence 2, Appl1
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12	84.5	8.0	53577	4	US-08-658-146-1 Sequence 1, Appl1

C 13	84	8.0	21706	4	US-08-961-527-36	Sequence 46, Appl1
C 14	81.5	7.7	3524	3	US-08-801-444-7	Sequence 7, Appl1
C 15	91.5	7.7	9524	4	US-09-459-696-7	Sequence 7, Appl1
C 16	80	7.6	3077	1	US-08-703-809-1	Sequence 1, Appl1
C 17	80	7.6	3077	1	US-08-703-808-1	Sequence 1, Appl1
C 18	80	7.6	3077	2	US-08-914-066-1	Sequence 1, Appl1
C 19	80	7.6	3077	2	US-08-703-807-1	Sequence 1, Appl1
C 20	80	7.6	3077	2	US-08-747-105A-1	Sequence 1, Appl1
C 21	80	7.6	3077	3	US-09-211-631-1	Sequence 1, Appl1
C 22	80	7.6	3077	4	US-05-555-528-1	Sequence 1, Appl1
C 23	80	7.6	3077	4	US-09-001-141-1	Sequence 1, Appl1
C 24	80	7.6	3077	4	US-05-532-803-1	Sequence 1, Appl1
C 25	80	7.6	3077	4	US-09-653-403-3	Sequence 3, Appl1
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C 32	79	7.5	7766	4	US-09-125-619-3	Sequence 3, Appl1
C 33	78.5	7.4	982	4	US-08-961-527-309	Sequence 309, Appl1
C 34	78	7.4	2153	2	US-08-861-801-2	Sequence 2, Appl1
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C 36	77	7.3	2344	1	US-07-695-472B-35	Sequence 35, Appl1
C 37	77	7.3	2347	1	US-08-250-740-32	Sequence 32, Appl1
C 38	77	7.3	2347	1	US-07-695-472B-1	Sequence 1, Appl1
C 39	77	7.3	2347	1	US-07-695-472B-34	Sequence 34, Appl1
C 40	77	7.3	2347	1	US-07-695-472B-36	Sequence 36, Appl1
C 41	77	7.3	15239	1	US-08-390-879-17	Sequence 17, Appl1
C 42	76.5	7.2	2249	2	US-08-860-635A-18	Sequence 18, Appl1
C 43	76.5	7.2	2249	4	US-09-281-476-18	Sequence 18, Appl1
C 44	76	7.2	1254	4	US-09-030-267-4	Sequence 4, Appl1
C 45	76	7.2	1316	1	US-08-579-667-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1

US-08-699-103B-1
Patent No. 5,574,242
Sequence 1, Application US/08699103B
GENERAL INFORMATION:
APPLICANT: Rine, Jasper D.
TITLE OF INVENTION: GENES AND PROTEINS CONTROLLING
FUNCTION OF INVENTION: GENES AND PROTEINS CONTROLLING
FUNCTION OF INVENTION: GENES AND PROTEINS CONTROLLING
PRIORITY CLAIM: 25
PUBLICATION ADDRESS:
ADDRESS: 4200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/699,103B
FILING DATE: 16-AUG-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/002,581
FILING DATE: 17-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/INVENT NUMBER: 09072005001
TELEPHONE/INFORMATION:
TELEPHONE: 650/322-5070
TELEFAX: 650/854-0875
INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 4982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA

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1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: DIKE, BRODSTEIN, ROBERTS & CASHMAN
 3 STREET: 130 WATER STREET
 4 CITY: BOSTON
 5 STATE: MA
 6 COUNTRY: USA
 7 ZIP: 02109
 8
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: Diskette
 11 COMPUTER: IBM Compatible
 12 OPERATING SYSTEM: DOS
 13 SOFTWARE: FASTSEQ Version 1.5
 14 CURRENT APPLICATION DATA:
 15 APPLICANT: KIMURA, YASUO
 16 FILING DATE: 22 MAR 1995
 17 CLASSIFICATION: 536
 18 PRIOR APPLICATION DATA:
 19 APPLICATION NUMBER: 08/254,494
 20 FILING DATE: 06 JUN 1994
 21 PRIOR APPLICATION DATA:
 22 APPLICATION NUMBER: JP-079996 1991
 23 FILING DATE: 12 APR 1991
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: JP-085396 1991
 26 FILING DATE: 14 APR 1991
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: JP 022321 1992
 29 FILING DATE: 07 FEB 1994
 30 ATTORNEY/AGENT INFORMATION:
 31 NAME: RESNICK, DAVID S.
 32 REGISTRATION NUMBER: 41777
 33 REFERENCE/WORK NUMBER: 41777
 34 TELEPHONE: (617) 523-3400
 35 TELEFAX: (617) 523-6440
 36 INFORMATION FOR SEQ ID NO: 1:
 37 SEQUENCE CHARACTERISTICS:
 38 LENGTH: 1120 base pairs
 39 TYPE: nucleic acid
 40 STRANDEDNESS: double
 41 TOPOLOGY: linear
 42 MOLECULE TYPE: cDNA to genomic RNA
 43 HYPOTHETICAL: NO
 44 ANTI-SENSE: NO
 45 FRAGMENT TYPE:
 46 ORIGINAL SOURCE:
 47 ORGANISM: human
 48 CELL TYPE: breast carcinoma
 49 CELL LINE: ZR-75-1
 50 NAME/KEY: Coding Sequence
 51 LOCATION: 112...795
 52 OTHER INFORMATION: E Mat peptide

Alignment Scores:
 1 Pred. No.: 0.015 Length: 1120
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 5 Query Match: 9.52% Indels: 44
 6 Gaps: 7

US-09-727-770-2 (1-205) x US-08-108-2226-3 (1-1120)

1 QY 80 AsnAspAspAspSerLeuTyrSerSerProLeuSerLeuValGlyLeuSerClyLeu 99
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 3 QY 100 AAtaAtaCpHeAAtaAbbValtIleValcIcAspHeCpIcTysScIcYlthAlaCIn 119
 4 Db 404 GAGAGCGGGGCCCTCATATGATGATGGTGGGTCTTCTGCGGTCTCTGCGAGAG 363

1 QY 120 ProAlaLeuPheValGlyMet - IleLeuIleLeuIlePheAla----- 133
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 3 QY 134 -----LysValIleIleLeuSerThrIysGlnProLeu 144
 4 Db 424 GCTGGGGGCAATCTGGGGGATATTTCACAAAGGATATAGCTGATTAAAGAAATCCAGAGTTT 483
 5 QY 145 SerCysProThrSerHisAlaIleArgGlySerLysAspHisProSerSerPheArgAsnGly 164
 6 Db 484 TACAAGGAATACATACAAAGCTGAAAAACAAAGAGATGAGCCGACAGAGGGGAAAGCGCTCAAA 543
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 8 Db 544 G---CAATGCTACTATGGCTTGAACCTGCTGCTGCTTGGCTGGGGGGGGTGGAAACAGT----- 595
 9 QY 178 LAspIleLeuSerValCileCysProArgValHisArgLeuLeuAlaArgCysProLeu 198
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 11 QY 198 uproPro 200
 12 Db 646 AAGTCTT 652

RESULT 7

US-08-254-493-3

1 Sequence 3, Application 08/08254493
 2 Patent No. 5439886
 3 GENERAL INFORMATION:
 4 APPLICANT: KIMURA, YASUO
 5 APPLICANT: KIMURA, YASUO
 6 APPLICANT: KIMURA, YASUO
 7 APPLICANT: KIMURA, YASUO
 8 TITLE OF INVENTION: PRODUCTION OF POLYPEPTIDES AND
 9 TITLE OF INVENTION: PRODUCTION THEREOF
 10 NUMBER OF SEQUENCES: 7
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: DIKE, BRODSTEIN, ROBERTS & CASHMAN
 13 STREET: 130 WATER STREET
 14 CITY: BOSTON
 15 STATE: MASSACHUSETTS
 16 COUNTRY: US
 17 ZIP: 02109
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk
 20 COMPUTER: IBM PC Compatible
 21 OPERATING SYSTEM: PC DOS/MS DOS
 22 SOFTWARE: Patent In Release #1.0, Version #1.25
 23 CURRENT APPLICATION DATA:
 24 APPLICATION NUMBER: US/08/254,493
 25 FILING DATE:
 26 CLASSIFICATION: 435
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: US 07/965552
 29 FILING DATE: 09-APR-1992
 30 PRIOR APPLICATION DATA:
 31 APPLICATION NUMBER: JP 079996-1991
 32 FILING DATE: 12-APR-1991
 33 PRIOR APPLICATION DATA:
 34 APPLICATION NUMBER: JP 085396-1991
 35 FILING DATE: 17-APR-1991
 36 PRIOR APPLICATION DATA:
 37 APPLICATION NUMBER: JP 022321-1992
 38 FILING DATE: 07 FEB 1992
 39 ATTORNEY/AGENT INFORMATION:
 40 NAME: RESNICK, DAVID S.
 41 REGISTRATION NUMBER: 41777
 42 REFERENCE/WORK NUMBER: 41777
 43 TELEPHONE: (617) 523-3400
 44 TELEFAX: (617) 523-6440
 45 TELEX: 200291 STEB UR
 46 INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; CELL TYPE: BREAST CARCINOMA
; CELL LINE: ZR-75-1
; FEATURE:
; NAME/KEY: GDS
; LOCATION: 112...795
; FEATURE:
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; LOCATION: 115...795
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Alignment Scores:

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US-09-727-770-2 (1-205) x US-08-254-493-3 (1-1120)

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||||| : : : : : ||||| : : : : :
DB 304 GAGAGCGCGCGCCCTCAAGATGCTGGTGCGGCTTCGCGGAGGCTGCGGAGAG 363
QY 120 ProArgLeuPheValGlyMet-----IleLeuIleLeuIlePheAla----- 133
||| : : : : : ||||| : : : : :
DB 364 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
QY 134 -----LysValIleLeuLeuSerThrLysGlnProLeu 144
||| : : : : :
DB 424 GTCGCGGCGCATCTGGGAGATTTCTGAAAGAGATGATTAAGGAAGTCTAGAGATT 483
QY 145 SerLysProThrSerHisAlaGlyAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 161
||| ||| : : : : : ||||| : : : : :
DB 484 TACAAGACACACCTACACACACCTCAAGATCAGTCCAGCGGCGGAGAGAGAGAGAG 543
QY 164 sGlnProAspThrHis ValLeuGlySerThrProSerValVa 179
||| ||| ||| : : : : : ||||| : : : : :
DB 544 G---CGATCGATGATGCTGTAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 595
QY 178 ValPheLeuSerValGlyGlySerAlaValHisAspLeuLeuAlaAlaAlaAlaAla 198
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DB 596 -----TTATCTCAGACATCTGCCCAAGA-----AGAGATATCGAAGACCTTCACAGG 645
QY 198 uProPro 200
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RESULT 6

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US-08-816-755-1

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; Sequence 1, Application US/08816755
; Patent No. 5847508

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GENERAL INFORMATION:

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; APPLICANT: Arleth, Anthony
; APPLICANT: Arnold, Anne
; APPLICANT: Shabon, Usman
; TITLE OF INVENTION: No. 5847508el Membrane Type Matrix
; TITLE OF INVENTION: Metalloproteinase-5 Gene
; NUMBER OF SEQUENCES: 6

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY:
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,755
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 4.45
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,444
; REFERENCE/EXCERPT NUMBER: CH50007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-816-755-1

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Alignment Scores:
Pred. No.: 2.01 Length: 4807
Score: 89.50 Matches: 54
Percent Similarity: 39.51% Conservat: 27
Best Local Similarity: 26.34% Mismatches: 56
Query Match: 8.48% Indels: 68
DB: 2 Gaps: 12

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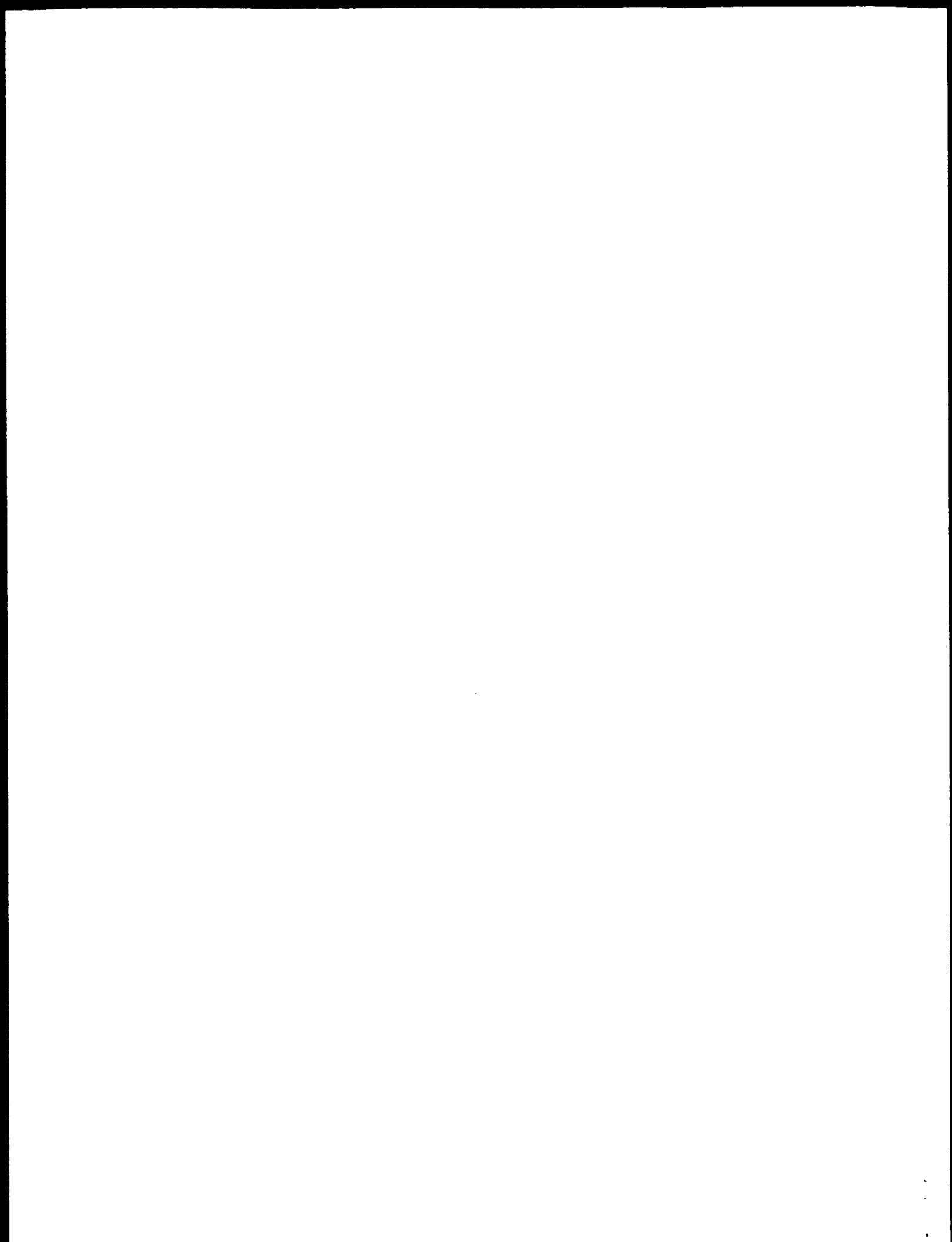
US-09-727-770-2 (1-205) x US-08-816-755-1 (1-4807)

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QY 49 -----GlyIleMetAlaMetSerValMetThrProGlnLeuIleHisMetLysSer 54
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DB 2965 GCGCTGGGAGCTGCTAAGCAAAATCTCTGTTCCTACAGCTGCTGCACTGGTTC 404
QY 55 IsoleuProValMetAlaGlyIleIleIleThrIleGlyGlyLeuValAlaValPro 74
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QY 75 ProAlaSerLeuAsnAspAspAsnSerLeuThrSerPheLeuGlnLeuGlyAla 94
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DB 3037 TGTTCATCATCTCTG-----TTTCTCTCATCTTCTGGGAAA 4072
QY 95 GlyLeuSerGlyLeuAlaAlaGlyPheAlaIleValIleValGlyAspThrGlyLysGly 114
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DB 3073 GGGAGG-----GTTCTGAG-----GTTCTGAG-----GTTCTGAG----- 4096
QY 115 GlyThrAlaGlnIleProArgLeu-----PheValIleMetIleLeuIleLeuIle 141
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DB 3097 -----GAACAATTGCGGAGATATTAGTGATTCATAGCTTTGCTATAC 4147
QY 122 PheAlaLysValLeuIle-----LeuSerThrLysGlnProGlnSerLysProThr 148
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DB 3148 TTGCAAAAGGACCTTTATAGCTACACCTGCTGCACTACAGAACTGCTTACGGGAT 4207

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Tue Dec 31 14:03:11 2002

JOURNAL Patent: WO 0194480-A 1 14-DEC-2001
 Applicant: Applera Corporation Robert A. Millman Assistant Secretary (US)
 FEATURES Location/Qualifiers
 1. 633
 /db_xref: "taxon:9606"
 BASE COUNT 128 a 202 c 154 g 150 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 6, 2c-148; Indels 0; Gaps 0;
 Matches 633; Conservative 0;
 QY 1 TCACAGAACATGTCACAAACAGCCGAGTAGTGTGTTTTCACCATCTCGAGTGT 60
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 QY 61 ATGGGACCATGTCACAGTGGCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 120
 Db 61 ATGGGACCATGTCACAGTGGCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 120
 QY 121 GGCATCATGCCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 180
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 Db 181 GTGGTATGCTGGTATGATCATCATCATCATCATCATCATCATCATCATCATCAT 240
 QY 241 TGGTCAATGATGACAAACAGTCTCTATAGAGTCTTCTCTAGTCTGGCTGGCT 300
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 QY 301 GGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 360
 Db 301 GGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 360
 QY 361 CAGCAGCGCGAGTATTTTGTAGTATGATGATGATGATGATGATGATGATGATGAT 420
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 QY 541 GTTGATCTCTTAAGTGTACAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
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 QY 601 CTCTGCGTCTGATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 633
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RESULT 2
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 DEFINITION AX347959
 VERSION AX347959.1 GI:18128675
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryote; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Li, Z., Wei, M.H., Kechum, K. and Heasley, E.M.
 TITLE Isolated human transporter proteins, nucleic acid molecules encoding human transporter proteins, and uses thereof

JOURNAL Patent: WO 0194480-A 1 14-DEC-2001
 Applicant: Applera Corporation Robert A. Millman Assistant Secretary (US)
 FEATURES Location/Qualifiers
 1. 633
 /db_xref: "taxon:9606"
 BASE COUNT 1613 a 1626 c 1609 g 1491 t
 ORIGIN

Query Match 98.9%; Score 626; DB 6; Length 6339;
 Best Local Similarity 100.0%; Pred. No. 4, 5c-146; Indels 0; Gaps 0;
 Matches 626; Conservative 0;
 QY 8 ACATGTCACAAACAGCCGAGTAGTGTGTTTTCACCATCTCGAGTGT 67
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 QY 68 CCATGTCACAGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCT 127
 Db 3058 CCATGTCACAGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCT 127
 QY 128 TGGCCATGTCATCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 187
 Db 3118 TGGCCATGTCATCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 187
 QY 188 TGGCTGCTATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 247
 Db 3178 TGGCTGCTATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 247
 QY 248 ATGATGACAAACAGTCTCTATAGAGTCTTCTCTAGTCTGGCTGGCTGGCT 307
 Db 3238 ATGATGACAAACAGTCTCTATAGAGTCTTCTCTAGTCTGGCTGGCTGGCT 307
 QY 308 CAGCGGCTTTGGCATGTCATCATCATCATCATCATCATCATCATCATCATCATCAT 367
 Db 3298 CAGCGGCTTTGGCATGTCATCATCATCATCATCATCATCATCATCATCATCATCAT 367
 QY 368 CCGCATATTGTAGGTCATCATCATCATCATCATCATCATCATCATCATCATCAT 427
 Db 3358 CCGCATATTGTAGGTCATCATCATCATCATCATCATCATCATCATCATCATCAT 427
 QY 428 CAAAGTACCGCTCTCTCAAAACAGTCTCTCAAAACAGTCTCTCAAAACAGTCTCT 487
 Db 3418 CAAAGTACCGCTCTCTCAAAACAGTCTCTCAAAACAGTCTCTCAAAACAGTCTCT 487
 QY 488 CATTCGGGACAAACAGTCTCTCAAAACAGTCTCTCAAAACAGTCTCTCAAAACAGT 547
 Db 3478 CATTCGGGACAAACAGTCTCTCAAAACAGTCTCTCAAAACAGTCTCTCAAAACAGT 547
 QY 548 TTCTAAGTGTACAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 607
 Db 3538 TTCTAAGTGTACAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 607
 QY 608 CCGATGCTGTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 633
 Db 3598 CCGATGCTGTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 633

RESULT 3
 LOCUS AC005973 Homo sapiens clone KIAA1173, w-4810, cDNA IMAGE, 20 ordered pieces.
 DEFINITION AC005973
 ACCESSION AC005973
 VERSION AC005973.7 GI:19225056
 KEYWORDS HTG, HTGS, PHASE2, HTGS, JAPANESE, HTGS, PHILIPINOS.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Homo sapiens, clone RP11-177H5

JOURNAL
REFERENCE
AUTHORS

Unpublished
2 (bases 1 to 151999)
Birken, B., Linton, J., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Baldwin, J., Barna, N., Beckel, J., Ben, J., Boutwell, C.,
Brown, A., Castle, A., Corry, T., Colapinto, M., Collins, S.,
Collins, A., Cooke, P., Corless, D., DePamphilis, M., DePamphilis, S.,
Donnell, J., Ferreira, P., FitzHugh, W., Forrest, C., Frenkel, K.,
Gale, D., Garg, S., Garg, S., Grant, C., Hargis, B., Heath, A.,
Horen, L., Horen, L., Jancz, J., Jones, C., Kunk, L.,
Karakas, A., Karkhanavala, P., Marquis, N., McKean, P.,
McKean, A., McKernan, K., Meltzer, J., Meltzer, W., Merrett, J.,
Myhalov, J., Nait, K., Naylor, J., Naylor, M., O'Connell, P.,
O'Donnell, P., Peltin, R., Peterson, K., Pyle, P., Roberts, D., Roy, A.,
Sever, P., Stach, S., Stach, S., Stach, S., Stach, S., Stach, S.,
Subramanian, A., Tachibana, N., Tachibana, N., Tachibana, N.,
Vassiliev, B., Vo, A., Waqar, A., Wheeler, J., Wu, Y., Wyman, D.,
Ye, W., Zhao, J., and Zody, M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Submitted (18-NOV-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 151999)

Birken, B., Linton, J., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Anderson, S., Barna, N., Beckel, J., Ben, J., Boutwell, C.,
Brown, A., Castle, A., Corry, T., Colapinto, M., Collins, S.,
Collins, A., Cooke, P., Corless, D., DePamphilis, M., DePamphilis, S.,
Donnell, J., Ferreira, P., FitzHugh, W., Forrest, C., Frenkel, K.,
Gale, D., Garg, S., Garg, S., Grant, C., Hargis, B., Heath, A.,
Horen, L., Horen, L., Jancz, J., Jones, C., Kunk, L.,
Karakas, A., Karkhanavala, P., Marquis, N., McKean, P.,
McKernan, K., Meltzer, J., Meltzer, W., Merrett, J.,
Myhalov, J., Nait, K., Naylor, J., Naylor, M., O'Connell, P.,
O'Donnell, P., Peltin, R., Peterson, K., Pyle, P., Roberts, D., Roy, A.,
Sever, P., Stach, S., Stach, S., Stach, S., Stach, S., Stach, S.,
Subramanian, A., Tachibana, N., Tachibana, N., Tachibana, N.,
Vassiliev, B., Vo, A., Waqar, A., Wheeler, J., Wu, Y., Wyman, D.,
Ye, W., Zhao, J., and Zody, M.

TITLE
JOURNAL
COMMENT

Submitted (07-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
on Mar 7, 2002 this sequence version replaced 41769674.
All repeats were identified using RepeatMasker.
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.protein.wisc.edu/ftp/1996/1997/

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 1485
Center clone name: 177_H5

----- Summary Statistics

Sequencing vector: pBluescript II (+/-), 100% of reads
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.960741
Consensus quality: 142221 bases at least Q40
Consensus quality: 145662 bases at least Q40
Consensus quality: 147521 bases at least Q20
Insert size: 138000; average 1p
Quality coverage: 4.5 to 920 bases; sum of contigs
Quality coverage: 4.0 to 920 bases; sum of contigs

* N.B. This is a working draft; extensive re-arranging
* consists of 20 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be revised.

1 41130: contig of 4110 bp in length
41131 41240: gap of 100 bp
41241 42274: contig of 1044 bp in length
42275 42374: gap of 100 bp
42375 44180: contig of 1806 bp in length
44181 44240: gap of 100 bp
44241 45329: contig of 1049 bp in length
45330 45429: gap of 100 bp
45430 47605: contig of 2176 bp in length
47606 47705: gap of 100 bp
47706 50517: contig of 2812 bp in length
50518 50617: gap of 100 bp
50618 54448: contig of 4831 bp in length
54449 54548: gap of 100 bp
54549 59069: contig of 4421 bp in length
59070 63587: gap of 100 bp
63588 63687: gap of 100 bp
63688 66665: contig of 4058 bp in length
66666 66765: gap of 100 bp
66766 71248: contig of 4483 bp in length
71249 71348: gap of 100 bp
71349 76193: contig of 4845 bp in length
76194 76293: gap of 100 bp
76294 86380: contig of 10037 bp in length
86381 86400: gap of 100 bp
86401 95039: contig of 8639 bp in length
95040 95139: gap of 100 bp
95140 102689: contig of 7550 bp in length
102690 102789: gap of 100 bp
102790 113821: contig of 11012 bp in length
113822 113901: gap of 100 bp
113902 122360: contig of 8459 bp in length
122361 122460: gap of 100 bp
122461 132544: contig of 10084 bp in length
132545 132644: gap of 100 bp
132645 147910: contig of 15266 bp in length
147911 148010: gap of 100 bp
148011 151999: contig of 4989 bp in length.

FEATURES

Source

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/db_xref="taxon:9606"
/clone "H11 177H5"

/clone_lib="RPG1-11 Human Male BAC"

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1. 41130
/note "assembly_fragment"
vector_end:SP6

misc_feature

41241..42274
/note="assembly_fragment"

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/note="assembly_fragment"

misc_feature

63608..66665
/note="assembly_fragment"

[illegible]

chemistry: dye-terminator Big Dye; 98% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 165221 bases at least Q40

Consensus quality: 176650 bases at least Q40

Consensus quality: 178768 bases at least Q20

Insert size: 20000, average 16

Insert size: 181495; sum-of-contigs

Quality coverage: 7.6 in Q20 bases

Note: This is a "working draft" sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence, as soon as it is available and the accession number will be preserved.

1 10663: contig of 10663 bp in length
* 10664 10763: gap of 100 bp
* 10764 11392: contig of 629 bp in length
* 11393 11492: gap of 100 bp
* 11493 12333: contig of 841 bp in length
* 12334 12433: gap of 100 bp
* 12434 13332: contig of 899 bp in length
* 13333 13432: gap of 100 bp
* 13433 14716: contig of 1284 bp in length
* 14717 14816: gap of 100 bp
* 14817 16101: contig of 1385 bp in length
* 16102 16201: gap of 100 bp
* 16202 17797: contig of 1595 bp in length
* 17798 17897: gap of 100 bp
* 17898 18493: contig of 1052 bp in length
* 18494 19049: gap of 100 bp
* 19050 20494: contig of 1445 bp in length
* 20495 20594: gap of 100 bp
* 20595 21775: contig of 1181 bp in length
* 21776 21875: gap of 100 bp
* 21876 24593: contig of 1584 bp in length
* 24594 25593: gap of 100 bp
* 25594 25831: contig of 2372 bp in length
* 25832 25931: gap of 100 bp
* 25932 27763: contig of 1832 bp in length
* 27764 27863: gap of 100 bp
* 27864 29986: contig of 2123 bp in length
* 29987 30086: gap of 100 bp
* 30087 32675: contig of 2589 bp in length
* 32676 32775: gap of 100 bp
* 32776 36266: contig of 3491 bp in length
* 36267 36366: gap of 100 bp
* 36367 39687: contig of 3321 bp in length
* 39688 39787: gap of 100 bp
* 39788 42811: contig of 3024 bp in length
* 42812 42911: gap of 100 bp
* 42912 47748: contig of 4837 bp in length
* 47749 47848: gap of 100 bp
* 47849 52056: contig of 4208 bp in length
* 52057 52156: gap of 100 bp
* 52157 56257: contig of 4101 bp in length
* 56258 56357: gap of 100 bp
* 56358 62635: contig of 6178 bp in length
* 62636 62735: gap of 100 bp
* 62736 65138: contig of 2503 bp in length
* 65139 65238: gap of 100 bp
* 65239 69640: contig of 4302 bp in length
* 69641 69740: gap of 100 bp
* 69741 74929: contig of 5198 bp in length
* 74930 74989: gap of 100 bp
* 74990 79482: contig of 4544 bp in length
* 79483 79582: gap of 100 bp
* 79583 81888: contig of 2306 bp in length
* 81889 81988: gap of 100 bp
* 81989 89859: contig of 7871 bp in length
* 89860 89959: gap of 100 bp
* 89960 158380: contig of 68421 bp in length

* 158381 158480: gap of 100 bp
* 158481 166923: contig of 8443 bp in length
* 166924 167023: gap of 100 bp
* 167024 176904: contig of 9881 bp in length
* 176905 177004: gap of 100 bp
* 177005 184595: contig of 7591 bp in length.

FEATURES

Location/Qualifiers

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/db_xref "taxon:9606"

/chromosome="17"

/map="17"

/clone="H31.91A22"

/clone_lib="RPCL11 Human Male BAC"

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clone_end:SP6

vector_side:left

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17898..18493

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/note="assembly_fragment"

52157..56257

/note="assembly_fragment"

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Best Local Similarity 100.0%; Freq. No. 3.4e-146; Indels 0; Gaps 0;

Matches 626; Conservative 0; Mismatches 0;

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QY 68 GATGTTGTCGATGAGTGGGTCGATGTTTGGTTTTCACATCTCGGGTGTATGGCA 127

|||||

DB 42118 GCAAGTGGTGAACAGCCCGGAGTATGTTTGGTTTTCACATCTCGGGTGTATGGCA 42177

QY 128 TGGCCATCTCTGTCATCTGCGCCAGAGTGTACCATATCAATCAATCCAGTGGCA 187

|||||

DB 42178 TGGCCATCTCTGTCATCTGCGCCAGAGTGTACCATATCAATCAATCCAGTGGCA 42237

TITLE	JOURNAL
Direct Submission Submitted (03-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
3 (bases 1 to 139484)	
Hirtten,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Bokuslavsky,I., Bonkhailter,B., Camarata,J., Chang,J., Chazaro,R., Choquet,Y., Collamore,A., Comar,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,D.S., Dodge,S., Faro,S., Ferretta,P., Fitzgerald,M., Gage,D., Galatun,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Jones,C., Kamat,A., Kerton,L., Holmes,W., Liye,I., Johnson,K., Jones,C., Landblad,T.H.K., Kartas,A., Kellis,C., Landers,L., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., MacDonald,P., Major,J., Matthews,A., McArthur,M., McElroy,J., Menon,S., Mihova,T., Mironov,V., Murphy,J., Nayler,J., Nelson,C., Nicol,K., Nodda,S., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Roman,J., Roy,A., Santoro,S., Schumacher,R., Seaman,S., Severin,P., Smith,C., Spencer,B., Stancu,Thomson,N., Stefanovic,N., Strauss,N., Testayo,S., Theodorou,J., Topham,K., Travis,N., Vassiliou,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zaiman,J., Zembek,L., Zimmer,A. and Zody,M.	
Center project name: 124553	
Center clone name: 115_H_24	
Center: Whitehead Institute/MIT Center for Genome Research Address: 320 Charles Street, Cambridge, MA 02141, USA On Aug 22, 2002, this sequence version replaced at: 2213470. All repeats were identified using RepeatMasker: Smith, A.F.A. & Green, P. (1996, 1997) http://ftp.cse.cmu.edu/pub/p124553/genome/masker.html	
Center code: WIRB Web site: http://www.genome.wi.mit.edu Contact: sequence submissions@genome.wi.mit.edu Project Information	
Center project name: 115_H_24	
Center clone name: 115_H_24	
NOTE: This is a working draft sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.	
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.	
1 13845: contig of 13845 bp in length	
* 13846 13945: gap of 100 bp	
* 13946 46401: contig of 32456 bp in length	
* 46404 46503: gap of 100 bp	
* 46504 50027: contig of 4524 bp in length	
* 50028 50127: gap of 100 bp	
* 50128 72136: contig of 22011 bp in length	
* 72139 72248: gap of 100 bp	
* 72249 95074: contig of 22876 bp in length	
* 95075 95174: gap of 100 bp	
* 95175 149384: contig of 44210 bp in length.	
tation/qualifiers	
1. 139384	
contigname "Homo sapiens"	
fileformat "fasta" / "genbank"	
chromosome "17"	
/map "17"	
clone "RP11-115H24"	
genome_lib "RefSeq Human Maple BAM"	
genome_id 33336 q 33819 c 35668 q 33810 t 751 others	
BASE COUNT 33336 a 33819 c 35668 g 33810 t 751 others	
ORIGIN	
Query Match 97.2% Score 615 E-22 Length 149484	
Best Local Similarity 99.8% Prod. No. 136 147	
Matches 626, Conservative 0, Mismatches 0, Indels 1, Gaps 1	

HMPCHSUA
LOCUS
DEFINITION: human vacuolar H+ ATPase proton channel submit mRNA, complete cds.
ACCESSION
VERSION M62762.1 GI:189675
KEYWORDS vacuolar H(+)-ATPase,
SOURCE Homo sapiens (tissue library: cDNA) cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Gillespie, G.A., Somlo, S., Germino, G.G., Weinstein, S., and
Mammalia; Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cpg Island in the region of an autosomal dominant polycystic kidney
disease locus defines the 5' end of a gene encoding a putative
proton channel
JOURNAL proc. Natl. Acad. Sci. U.S.A. 88 (10), 4289-4293 (1991)
MEDLINE 91249553
PubMed 1709739
FEATURES
Location/Qualifiers
1..1162
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="16p13.4"
/cell_type="Bcell"
/tissue="lib "cdna"
1..1162
/gene="ATP1"
231..698
/gene="ATP1"
/codon_start=1
/product="vacuolar H+ ATPase proton channel subunit"
/protein_id="AA060049.1"
/db_xref="GI:189675"
/db_xref="GB:G00128-131"
2:translation "MSPSKSGDEYASPEAVMIAASAAVFSAIAAAGTAKSGTIGIAAM
SVMRPQIMKSLIVVMAGLIALYGLVAVLIANSINDDLSLYKSFQLGAGLSVGLS
GLAAGFATIGVAGVRGTAQDRLFVGMILLIPAEVLGLGLVALLLSIK"
BASE COUNT 185 a 383 c 282 g 228 t
ORIGIN

Query Match 59.0%; Score 374.4; DB 9; Length 1078;
Best Local Similarity 78.2%; Pred. No. 6,60-83;
Matches 517; Conservative 0; Mismatches 101; Indels 43; Gaps 4;
QY 12 GTGCAACACAGGCGGAGTATGCTTTGGTTTCACATCTCGGGTGTATGCCACCAT 71
DB 124 GTGCAACAGGCGGAGTATGCTTTGGTTTCACATCTCGGGTGTATGCCACCAT 183
QY 72 GGTCTGACATGGGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 131
DB 184 GGTCTGACATGGGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 243
QY 132 CATGCTGTATGTCGCGGAGGAGTATGTCATGATGATGATGATGATGATGATGATG 191
DB 244 CATGCTGTATGTCGCGGAGGAGTATGTCATGATGATGATGATGATGATGATGATG 300
QY 192 TGGTATATCAT 251
DB 301 TGGTATATCAT 360
QY 252 TGACAGAGGCTCTATAGAGTATTCGTCGAGCTGGGCTGGGCTGGGCTGGGCTGGG 299
DB 461 CGACATGAGGCTCTATAGAGTATTCGTCGAGCTGGGCTGGGCTGGGCTGGGCTGGG 420
QY 300 TGGCTGAGGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 359
DB 421 CGGCTGAGGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 480
QY 360 CGACAGGAGGAGTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 414
DB 481 CGACAGGAGGAGTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 415 -----CPCATCTCTGTCACAAAGCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 452
DB 541 GCTCTAGGCT 600
QY 453 CAGTCACAGATATAGATTAAGAGCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 512
DB 601 CAGTCACAGATATATATGTAAGAGCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
QY 513 GATCTGTCTGAGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 572
DB 661 ATACGAGGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 719
QY 573 TCACTGTCTGAGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 632
DB 720 CCACTGTCTGAGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 779
QY 633 C 633
DB 780 C 780
RESULT 10

XX Li Z, Wei M, Ketchum K, Beasley EM;
 XX WPI: 2002-566438/60.
 XX P-PSDB: AA015455.
 XX New human transporter proteins related to the proton ATPase transporter
 XX subfamily for diagnosing and treating diseases mediated by the
 XX transporter protein and for identifying modulators
 XX Claim 23; Fig 1; 70pp; English.
 XX The invention comprises the amino acid and coding sequence of a human
 XX transporter protein. Transporter proteins regulate many different
 XX functions of a cell, including cell proliferation, differentiation and
 XX signalling processes. Transporter proteins function by regulating the
 XX flow of molecules such as ions and macromolecules into and out of cells.
 XX The gene for the human transporter protein is located on chromosome 17.
 XX The DNA and protein sequences of the invention are useful for identifying
 XX agents that modulate or bind to the human transporter protein. The DNA
 XX and protein sequences are useful for treating a disease or condition that
 XX is mediated by a human transporter protein. The DNA and protein sequences
 XX of the invention may also be used in the construction of transgenic
 XX animals, pharmacogenomic analysis and for tissue typing. The present DNA
 XX sequence encodes the human transporter protein of the invention.
 XX Sequence: 633 bp; 128 A; 202 C; 153 G; 150 T; 0 other;
 SQ
 Query Match 100.0%; Score 633; DB 24; Length 633;
 Best Local Similarity 100.0%; Pred. No. 6,8e 176;
 Matches 633; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCACAGACATGCGGCAACAGACAGCCGAGATAGCTTTGCTTTTCACATCTCGGCTCT 60
 DB 1 TCACAGACATGCGGCAACAGACAGCCGAGATAGCTTTGCTTTTCACATCTCGGCTCT 60
 QY 61 ATGCGGACATGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 DB 61 ATGCGGACATGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 121 GCGATGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 121 GCGATGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 181 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 181 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 TCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 241 TCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 301 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 301 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 361 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 361 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 421 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 481 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 DB 481 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 541 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 541 GCGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 601 CTCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 633

DB 601 CTCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

RESULT 2

AA015455 standard: DNA: 633 bp.

XX AAL44086;

XX AAL44086;

XX 03-OCT-2002 (first entry)

XX Human transporter protein gene sequence.

XX Human: gene, ds; gene therapy; transporter protein; cell proliferation;
 XX cell differentiation; cell signalling; chromosome 17; transgenic animal;
 XX transporter protein-mediated disease; pharmacogenomic analysis;
 XX tissue typing.

XX Homo sapiens.

XX key location/qualifiers

XX variation replace (55%, A)

XX /tag a

XX /standard_name "Single nucleotide polymorphism"

XX /note "The present base is optionally absent"

XX 3000..3617

XX /tag b

XX /product "Human transporter protein"

XX variation replace (46.48, C)

XX /tag c

XX /standard_name "Single nucleotide polymorphism"

XX variation replace (54.46, T/C)

XX /tag d

XX /standard_name "Single nucleotide polymorphism"

XX variation replace (58.08, G)

XX /tag e

XX /standard_name "Single nucleotide polymorphism"

XX variation replace (58.92, C)

XX /tag f

XX /standard_name "Single nucleotide polymorphism"

XX variation replace (60.71, G)

XX /tag g

XX /standard_name "Single nucleotide polymorphism"

XX W0200194380-A2.

XX PN

XX 13-DEC-2001.

XX 31-MAY-2001; 2001WO-0517511.

XX 02 JUN 2000; 200005-2688560.

XX 04 DEC 2000; 2000US-0727770.

XX (APPL-) APPLERA CORP.

XX Li Z, Wei M, Ketchum K, Beasley EM;

XX WPI: 2002-566438/60.

XX P-PSDB: AA015455.

XX New human transporter proteins related to the proton ATPase transporter
 XX subfamily for diagnosing and treating diseases mediated by the
 XX transporter protein and for identifying modulators

XX Claim 23; Fig 1; 70pp; English.

XX The invention comprises the amino acid and coding sequence of a human
 XX transporter protein. Transporter proteins regulate many different
 XX functions of a cell, including cell proliferation, differentiation and
 XX signalling processes. Transporter proteins function by regulating the
 XX flow of molecules such as ions and macromolecules into and out of cells.
 XX The gene for the human transporter protein is located on chromosome 17.

PK 04-FEB-2000; 2000US-0180412.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 04-AUG-2000; 2000US-0632466.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236459.
 PR 04-OCT-2000; 2000US-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 FI Penn SG, Hanzel BK, Chen W, Rank DR;
 XX
 BK WPI, 2001 18895573
 XX
 PT Single exon nucleic acid probe for analyzing gene expression in human
 PI hearts -
 XX
 PS Claim 4: SEQ ID NO 10036; 540pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human hearts. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging,
 CC monitoring and prognosing diseases of the human heart and vascular system
 CC such as cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at http://wpi.int/pub/published/pub_sequence.
 XX
 SS Sequence 612 BP; 120 A; 195 C; 151 G; 146 T; 0 other;

Query Match 96.7%; Score 612; DB 22; Length 612;
 Best Local Similarity 100.0%; Pred. No. 9,9e-170;
 Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YY 8 ACATGTCGTAACACAGCGGAGATGCTTTGTTTTCATCATCTGGGGTCTATGCGCA 67
 BB 1 ACATGTCGTAACACAGCGGAGATGCTTTGTTTTCATCATCTGGGGTCTATGCGCA 60
 YY 68 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 127
 BB 61 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 120
 YY 128 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 187
 BB 121 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 180
 YY 188 TGGTGTATATCATCATCATATATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 247
 BB 181 TGGTGTATATCATCATCATATATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 240
 YY 248 ATGATGACACACATCTCTATACAGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 297
 BB 241 ATGATGACACACATCTCTATACAGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 300
 YY 308 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 367
 BB 301 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 360
 YY 408 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 427
 BB 361 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 420
 YY 428 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 487
 BB 421 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 480
 YY 488 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 547
 BB 481 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 540

YY 548 TCTAAGTGTACAGTGTCT 607
 BB 541 TCTAAGTGTACAGTGTCT 600
 YY 608 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 619
 BB 601 CCAATGTCGTCAGTGGCTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 612

RESULT 6

AAK12891
 LC AAK12891 standard, LNA, 612 BP.

XX AAK12891;

XX 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe SEQ ID NO: 12882.

XX Human, brain expressed exon, gene expression analysis, probe;
 KW microarray; Alzheimer's disease, multiple sclerosis, schizophrenia;
 KW epilepsy, cancer; SS.

XX Homo sapiens.

XX WU00157275 A2.

XX 09-AUG-2001.

XX 30 JAN 2001; 2001WO 0300667.

XX 04 FEB 2000; 2000US 0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03 AUG 2000; 2000US 0642366.

XX 21 SEP-2000; 2000US 0244687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000US-0024264.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel BK, Chen W, Rank DR;

XX WPI, 2001 18895573.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX brains -

XX Example 4: SEQ ID NO: 12882; 650pp; Sequence listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX brain. They can be used to measure gene expression in brain cell samples,

XX which may enable the diagnosis and improved treatment of nervous system

XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX epilepsy and cancers. The present sequence is one of the probes of the

XX invention.

XX Sequence 612 BP; 120 A; 195 C; 151 G; 146 T; 0 other;

XX Query Match 96.7%; Score 612; DB 22; Length 612;

XX Best Local Similarity 100.0%; Pred. No. 9,9e-170;

XX Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Dec 31 14:03:11 2002

DT 01-FEB-2002 (first entry)
 XX Human fetal liver single exon nucleic acid probe #58.
 DE Human, fetal liver, gene expression; single exon nucleic acid probe; ss.
 KW Homo sapiens.
 OS Homo sapiens.
 PN W0200157277-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-0800669.
 XX 04-FEB-2000; 2000US-0140312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632466.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-484447/52.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver.
 XX Claim 1: SEQ ID NO 58; 639pp + sequence listing; English.
 PS The invention relates to a single exon nucleic acid probe for
 XX measuring human gene expression in a sample derived from human fetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a single exon nucleic acid
 CC probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 XX Sequence 448 bp; 79 A; 147 C; 112 G; 110 T; 0 other;
 SQ
 Query Match 59.2%; Score 475; DP 22; Length 448;
 Best Local Similarity 100.0%; Prod. No. 40-100;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 ACATGTCACCAACACGCGAGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 67
 DB 74 ATATGTCACCAACACGCGAGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 133
 QY 68 CCATGTCACCAACACGCGAGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 127
 DB 134 CCATGTCACCAACACGCGAGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 193
 QY 128 TCGGTAATGTCATCATCTCGGGTGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 187
 DB 194 TCGGTAATGTCATCATCTCGGGTGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 253
 QY 188 TCGGTAATGTCATCATCTCGGGTGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 247
 DB 254 TCGGTAATGTCATCATCTCGGGTGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 313
 QY 248 ATGATGACACACATCTCTATAGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 307
 DB 314 ATGATGACACACATCTCTATAGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 373
 QY 308 CAGCGGCGCTTTGCGATGCTATGCTTTTCATCATCTCGGGTGTATATGCGCA 367
 DB 374 CAGCGGCGCTTTGCGATGCTATGCTTTTCATCATCTCGGGTGTATATGCGCA 433

QY 368 CCGCCTATTGTTAG 482
 DB 434 CCGCCTATTGTTAG 448
 RESULT 13
 ABA21582
 ID ABA21582 standard; DNA; 448 bp.
 XX ABA21582;
 AC ABA21582;
 XX 23-JAN-2002 (first entry)
 XX Probe #48 for gene expression analysis in human heart cell sample.
 DE Human; gene expression; heart; arrhythmia; cardiovascular system; prod;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 XX congenital heart disease; ss.
 OS Homo sapiens.
 XX W0200157274-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-0800669.
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632466.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX Claim 1: SEQ ID NO 48; 530pp; English.
 PS The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, studying, treating,
 CC monitoring and prognosis of diseases of the human heart and vascular system
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.
 XX Sequence 448 bp; 79 A; 147 C; 112 G; 110 T; 0 other;
 SQ
 Query Match 59.2%; Score 475; DP 22; Length 448;
 Best Local Similarity 100.0%; Prod. No. 40-100;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 ACATGTCACCAACACGCGAGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 67
 DB 74 ACATGTCACCAACACGCGAGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 133
 QY 68 CCATGTCACCAACACGCGAGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 127
 DB 134 CCATGTCACCAACACGCGAGTATGCTTTTCATCATCTCGGGTGTATATGCGCA 193

QY 128 TGGTAATGCTGTCATGAGTGGACAGCTCATCTACAGCAAGATCCATCATCCACTGCTCA 187
 DB 144 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 193
 QY 188 TGGCTGATATCATCAATCAT 247
 DB 254 TGGCTGATATCATCAATCAT 313
 QY 248 ATGATGACAAATCTCTCTATATAGCAATTTCTCTAGTGGAGAGCTGAGCTGAGCTGG 307
 DB 314 ATGATGACAAATCTCTCTATATAGCAATTTCTCTAGTGGAGAGCTGAGCTGAGCTGG 373
 QY 308 CAGCGCGCTTTGTCATGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
 DB 374 CAGCGCGCTTTGTCATGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
 QY 468 CCGGACATTTGTAG 482
 DB 434 CCGGACATTTGTAG 448
 RESULT 14
 AAK03062
 ID AAK03062 standard, DNA, 448 BP.
 AC AAK03062;
 XX 05-NOV-2001 (first entry)
 DE Human brain expressed single exon probe SEQ ID NO: 53.
 KW Human brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer; ss.
 OS Homo sapiens.
 XX
 PN W0200157275-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-0500667.
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234697.
 PR 27-SEP-2000; 2000US-0234659.
 PR 04-OCT-2000; 2000US-0024263.
 XX (M I E) MOLECULAR DYNAMICS INC.
 PA Penn SD, Hanzel WK, Chen W, Rank DR;
 XX WPI, 2001-483446/52.
 DE Single exon nucleic acid probes for analyzing gene expression in human
 XX brains -
 XX Example 4; SEQ ID NO: 53; 450pp + Sequence Listing; English
 XX The present invention provides a number of single exon nucleic acid
 XX probes which are derived from genomic sequences expressed in the human
 XX brain. They can be used to measure gene expression in brain cell samples,
 XX which may enable the diagnosis and improved treatment of nervous system
 XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 XX epilepsy and cancers. The present sequence is one of the probes of the
 XX invention
 XX
 SE Sequence 448 BP; 79 A; 147 G; 112 C; 110 T; 6 other
 Query Match 59.2% Query 176 300 22 14983 419.

Host Local Similarity 100.0%; Prod. No. 4c-100;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 ACAATGCAACAAACAGAGAGAGATAGCTTTGGTTTTCACATCTGGTGTGATGATCA 57
 DB 74 ACAATGCAACAAACAGAGAGATAGCTTTGGTTTTCACATCTGGTGTGATGATCA 133
 QY 68 CCAATGCTTCCATGAGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 127
 DB 134 CCAATGCTTCCATGAGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 193
 QY 128 TGGCTGATATCATCAATCAT 187
 DB 194 TGGCTGATATCATCAATCAT 253
 QY 188 TGGCTGATATCATCAATCAT 247
 DB 254 TGGCTGATATCATCAATCAT 313
 QY 248 ATGATGACAAATCTCTCTATATAGCAATTTCTCTAGTGGAGAGCTGAGCTGAGCTGG 307
 DB 314 ATGATGACAAATCTCTCTATATAGCAATTTCTCTAGTGGAGAGCTGAGCTGAGCTGG 373
 QY 308 CAGCGCGCTTTGTCATGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
 DB 374 CAGCGCGCTTTGTCATGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
 QY 468 CCGGACATTTGTAG 482
 DB 434 CCGGACATTTGTAG 448
 RESULT 15
 AAK25499
 ID AAK25499 standard, DNA, 448 BP.
 AC AAK25499;
 XX 06-NOV-2001 (first entry)
 DE Human bone marrow expressed single exon probe SEQ ID NO: 56.
 KW Human bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukemia; lymphoma; myeloma; ss.
 OS Homo sapiens.
 XX
 PN W0200157276-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-0500668.
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234697.
 PR 27-SEP-2000; 2000US-0234659.
 PR 04-OCT-2000; 2000US-0024263.
 XX (M I E) MOLECULAR DYNAMICS INC.
 PA Penn SD, Hanzel WK, Chen W, Rank DR;
 XX WPI, 2001-483446/53.
 DE Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human bone marrow -
 XX Example 4; SEQ ID NO: 56; 958pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid

Tue Dec 31 14:03:11 2002

us-09-727-770-1.rng

cc probes which are derived from genomic sequences expressed in the human
cc bone marrow. They can be used to measure gene expression in bone marrow
cc samples, which may enable the improved diagnosis and treatment of cancers
cc such as lymphoma, leukemia and myeloma. The present sequence is one of
cc the probes of the invention.

xx
SQ Sequence 448 bp; 79 A; 147 C; 112 G; 110 T; 0 other;

Query Match	59.28;	Score 375;	DB 22;	Length 448;
Best Local Similarity	100.00;	Pred. No. 4e-100;		
Matches 375;	Conservative 0;	Mismatches 0;	Indels 0;	Caps 0;

QY	8	ATATGTCACAAACAGCGCGAGTATGCTTTGGTTTTCACCATCTCTCGGGTGTATGCGCA	67
DB	74	ACATGTCACAAACAGCGCGAGTATGCTTTGGTTTTCACCATCTCTCGGGTGTATGCGCA	143
QY	68	CCATGGTCTCCAGTGGCGCTGGGTGCTGGCTGTGATGGTCAAGAAATGGCACCGGATCA	127
DB	134	CCATGGTCTCCAGTGGCGCTGGGTGCTGGCTGTGATGGTCAAGAAATGGCACCGGATCA	193
QY	128	TGGTCATGCTGTCTATGTCGGCCAGAGTATGATGACATGAAGTCCATCATCCACAGTGTCA	187
DB	194	TGGTCATGCTGTCTATGTCGGCCAGAGTATGATGACATGAAGTCCATCATCCACAGTGTCA	253
QY	188	TGGCTGGTATCATCACCATCTATGGCCCTAGTGGCGGCTGTCTCGCCCTGCCAACCTCGTGA	247
DB	254	TGGCTGGTATCATCACCATCTATGGCCCTAGTGGCGGCTGTCTCGCCCTGCCAACCTCGTGA	313
QY	248	ATGATGACAAACAGTCTCTATAGTAGTTCCTCCAGCTGGGAGGTGGGCTGAGTGGCGTGG	307
DB	314	ATGATGACAAACAGTCTCTATAGTAGTTCCTCCAGCTGGGAGGTGGGCTGAGTGGCGTGG	373
QY	408	CAGCGAGGCTTTGGCATCTGCTATGCTGGGGACACTGGCAAGTGTGCACTGCCGACGAGG	367
DB	474	CAGCGAGGCTTTGGCATCTGCTATGCTGGGGACACTGGCAAGTGTGCACTGCCGACGAGG	433
QY	368	CCGACTATTGTGAG	382
DB	434	CCGACTATTGTGAG	448

Search completed: December 28, 2002, 09:49:05
Job time : 266 secs

GenBank version: 5.1.2
Copyright (c) 1993 - 2002 Computer Ltd.

OM nucleotide - nucleotide search, using sw model

Run on: December 28, 2002, 09:22:31 - Search time 1982 seconds
(without alignments)
5169.815 Million cell updates/sec

Title: us-09-727-770-1
Perfect score: 633
Sequence: 1 tcaagagacatgcaacaa.....ctgagacatctgaactac 633

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 809743376 residues

Total number of hits satisfying chosen parameters: 20000000

Minimum DB seq length: 0

Maximum BP seq length: 20000000

Post-processing: Minimum Match 0
Maximum Match 100
Listing first 45 summaries

Database: EST

- 1: em_estba:*
- 2: em_estum:*
- 3: em_estin:*
- 4: em_estma:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_estc:*
- 9: db_est1:*
- 10: db_est2:*
- 11: db_est3:*
- 12: db_est4:*
- 13: db_est5:*
- 14: db_est6:*
- 15: em_estom:*
- 16: db_est7:*
- 17: db_est8:*
- 18: em_oss_hum:*
- 19: em_oss_inv:*
- 20: em_oss_pln:*
- 21: em_oss_vrt:*
- 22: em_oss_fun:*
- 23: em_oss_mam:*
- 24: em_oss_mus:*
- 25: em_oss_other:*
- 26: em_oss_pro:*
- 27: em_oss_ror:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	375	59.2	908	14	BQ722145
2	375	59.2	981	14	BQ678034
3	375	59.2	1091	14	BQ232887
4	373.4	59.0	993	14	BQ463421
5	373.4	59.0	1063	14	BQ054546
6	371.8	58.7	922	14	BQ121511

7	371.8	58.7	1076	14	BQ229395
8	369.6	58.4	986	14	BQ23102
9	369.6	58.4	991	14	BQ918449
10	368.6	58.2	1076	13	BQ544498
11	368.2	58.2	1222	13	BQ478359
12	363	57.3	696	14	BQ791193
13	362.9	57.3	928	14	BQ279185
14	362.9	57.3	1061	13	BQ562656
15	361.8	57.2	1031	13	BQ554691
16	360.2	56.9	996	14	BQ058594
17	360	56.9	1093	13	BQ547917
18	359.8	56.8	991	9	AL552414
19	359.4	56.8	908	14	BQ224964
20	358.8	56.7	1201	14	BQ474665
21	357.8	56.7	872	14	BQ232398
22	357.5	56.5	883	14	BQ719173
23	353	55.8	631	14	BQ769410
24	353	55.8	634	14	BQ843350
25	353	55.8	638	14	BQ818948
26	353	55.8	657	14	BQ769872
27	349.6	55.2	995	14	BQ521094
28	348.6	55.1	1092	13	BQ452233
29	348.2	55.0	1136	13	BQ554912
30	347.6	54.9	941	12	BQ697438
31	347.6	54.9	913	14	BQ949611
32	347.4	54.9	907	14	BQ879221
33	346.6	54.8	722	12	BQ797916
34	345.8	54.6	1017	13	BQ549877
35	345.6	54.6	821	9	AL552541
36	345.6	54.6	969	14	BQ060051
37	345.6	54.6	1169	14	BQ928304
38	344.8	54.5	921	9	AL552453
39	344.4	54.4	670	12	BQ741415
40	343.4	54.2	936	14	BQ919999
41	343.2	54.2	904	14	BQ218416
42	342	54.0	682	12	BQ831575
43	341.2	53.9	1104	14	BQ924578
44	338.2	53.4	645	10	AW514320
45	336.4	53.1	869	9	AL575876

ALIGNMENTS

RESULT 1
BQ722145
Locus: 908 bp: mRNA linear EST 16 JUN 2002
DEFINITION: AGRICULT_8294578 lupski_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6194244 5', mRNA sequence.
ACCESSION: BQ722145
VERSION: BQ722145.1 GI:21861042
KEYWORDS: EST.
SOURCE: human.
ORGANISM: Homo sapiens

REFERENCE: 1 (bases 1 to 908)
AUTHORS: NIH-MDC help2seq seq web server.
TITLE: National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL: Unpublished (1999)
COMMENT: Contact: Robert Stransberg, Ph.D.
Email: rstransb@mail.nih.gov

PROB. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

us-09-727-770-1.rst
cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the L.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13599 row: c column: 13
High quality sequence stop: 644.
Location/Qualifiers
1: 908

us-09-727-770-1.rst

Tue Dec 31 14:03:12 2002

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/db_xref: "taxon:9606"
/clone: "IMAGE:414244"
/clone_lib: "topski_sympathetic_trunk"
/sex: "male"
/tissue_type: "sympathetic trunk"
/dev_stage: "adult, 16 yr"
/lab_host: "pH10R"
/notes: "Vector: pCMV-Sport6 (Life Technologies); Site_1:
Note1: Site 2: Salt; cDNA made by oligo-dT priming;
directionally cloned using the following adaptors:
5'-TGCACGACGAGGCTG-3' and
5'-GATATCTTCTATGAGGAGGAGGAGGCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a partial
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupecki, M.D., Ph.D. (aylor
College of Medicine); available through Life
Technologies."
BASE COUNT      14 a  311 c  248 q  200 t
ORIGIN
Query Match      59.2%; Score 375; DB 14; Length 908;
Best Local Similarity 78.4%; Pred. No. 6, 5e-87;
Matches 518; Conservative 0; Mismatches 100; Indels 43; Gaps 4;
QY 12 GTCTAACACACGCGGAGTATGCTTTGTTTTCACCAATCTGCTGCTATATGGGCAAT 71
Db 27 GTCCAAAGACGCGCGGAGTATGCTTTGTTTTCACCAATCTGCTGCTATATGGGCAAT 86
QY 72 GGTCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 131
Db 87 GGTCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 146
QY 132 CAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 191
Db 147 CAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
QY 192 TGTATATCATCAGCATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
Db 204 TGGCATATCCGACATCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 263
QY 252 TGACCAACACTGCTTATAGCAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 299
Db 264 GGACATCAGGCTCTACAAAGACTTCCCTCCAGCTGGGCGGCTGAGGCTGGGCTGAG 323
QY 300 TGGGCTGCGAGCGCGCTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
Db 324 CGGCTGCGAGCGCGCTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 383
QY 360 CGAGCGCGCGGACTATTTGCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 414
Db 384 CGAGCGCGCGGACTATTTGCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443
QY 415 -----CTCATCTCTCCACAAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 452
Db 444 CCGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503
QY 453 CAGTCACAGATACGATGTAAGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
Db 504 CAGTCACAGATACGATGTAAGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563
QY 513 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
Db 564 ATAGAGAGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 622
QY 573 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
Db 623 CAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 682
QY 633 C 633
Db 683 C 683

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RESULT 2
R0678034
LOCUS      981 bp      mRNA      linear      EST 15 JUL 2002
DEFINITION AGINGC0001_R034321 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:414082
5', mRNA sequence.
R0678034
R0678034.1 G1:21790713
EST
human.
SOURCE      Homo Sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 981)
AUTHORS     NIH MGC staff; Macgregar S, et al.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Submitted (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
Email: rstraus@nsl.nih.gov
Tissue procurement: JET/IDP
cDNA library preparation: Rubin Laboratory
cDNA library Arrayed by: The M.A.C.E. Consortium (JRL)
DNA Sequencing by: Amersham Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the M.A.C.E. Consortium/JRL at:
http://image.llnl.gov
plate: 11/M2380 row: n column: 04
high quality sequence stop: 709.
Location/Qualifiers
1..981
/organism: "Homo sapiens"
/db_xref: "taxon:9606"
/clone: "IMAGE:414082"
/clone_lib: "NIH_MGC_112"
/tissue_type: "melanotic melanoma, cell line"
/lab_host: "pH10R (phage resistant)"
/notes: "Organ: skin; Vector: pTZ19; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo dT priming. directionally cloned
into pCDR1/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Lind Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."
BASE COUNT      158 a  353 c  263 q  207 t
ORIGIN
Query Match      59.2%; Score 375; DB 14; Length 981;
Best Local Similarity 78.4%; Pred. No. 6, 5e-87;
Matches 518; Conservative 0; Mismatches 100; Indels 43; Gaps 4;
QY 12 GTCCACACACGCGCGGAGTATGCTTTGTTTTCACCAATCTGCTGCTATATGGGCAAT 71
Db 97 GTCCACAGCGCGCGGAGTATGCTTTGTTTTCACCAATCTGCTGCTATATGGGCAAT 106
QY 72 GGTCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 141
Db 157 GGTCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 216
QY 142 CATGCTCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 191
Db 217 CATGCTCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 273
QY 192 TGGATCATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
Db 274 TGGATCATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333
QY 252 TCACCAACACTGCTTATAGCAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 299
Db 334 CGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399
QY 300 TGGGCTGCGAGCGCGCTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359

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[illegible]

[illegible]

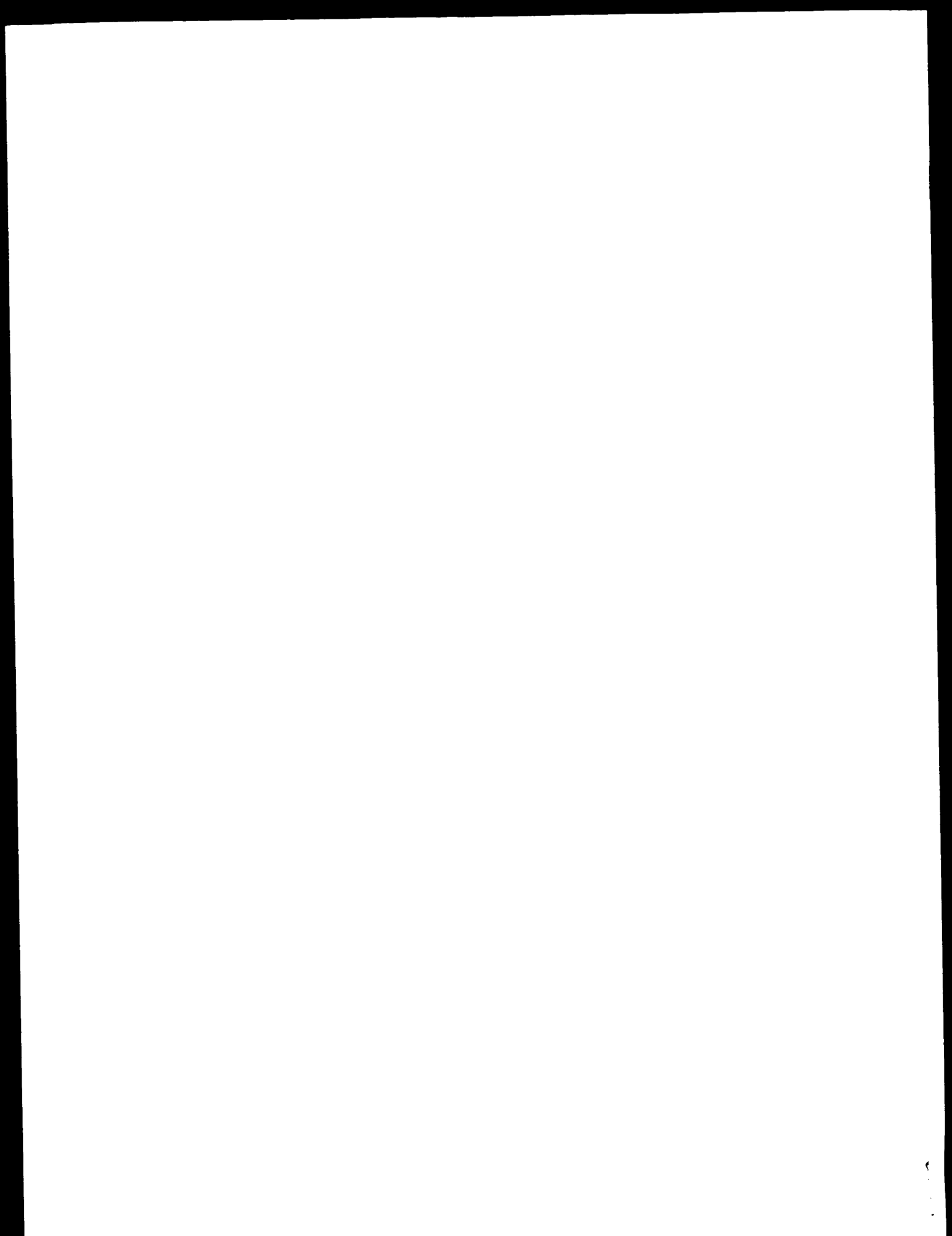
National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Stransberg, Ph.D.
 Email: equips_email.nih.gov
 Tissue Procurement: APC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (I.M.I.)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 accessed through the I.M.A.G.E. Consortium/I.M.I. at:

normalized and enriched for full length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code: 012."									
SE count	192 g	393 c	275 q	225 t	1 others				
1Q1N									
Query Match	58.2%	Score	468.6;	Dk	13; Length	1076;			
Best Local Similarity	77.8%;	pred.	No.	3,1e+85;					
Mismatches	514;	Conservative	0;	Mismatches	104;	Indels	4;	Gaps	4;

SEE COUNT
101N

Query Match 57.3% Score 362.4; DB 14; Length 928;
Best Local Similarity 78.3% Pred. No. 9,50-84;
Matches 504; Conservative 0; Mismatches 97; Indels 43; Gaps 4;
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156 GTCCACACACAGTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGGACATAT 156
72 GATCTTCAGTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGGACATAT 131
157 GATCTTCAGTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGGACATAT 216
122 CATGTCTGTGATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 191
217 CATGTCTGTGATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 273
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334 GCACACAGTGTGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 393
300 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 359
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453 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 512
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573 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 616
693 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 736
RESULT 14
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DEFINITION ACENSGRBT656751 NIH_MGC_1107 Homo sapiens cDNA clone IMAGE:5746584
5' mRNA sequence.
ACCESSION BM562656
VERSION BM562656.1 GI:18808940
FEATURES
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Cladocera; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1061)
NIH_MGC_1107: Mammalian Gene Collection (MGC)
National Institutes of Health
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rasb@nsl.jhu.edu
Tissue Procurement: APEC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Amersham Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Map: L1AM12745 row: 1 column: 09
High quality sequence stop: 703.
Location/Qualifiers
1..1061
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Zusatz "IMAGE:5746584"
Zusatz "NIH_MGC_1107"
Zusatz "dendritic adenocarcinoma, cell line"
Zusatz "pH10H (phage-resistant)"
Zusatz "organ: small intestine; Vector: pMW Short6;
Site 1: Not; Site 2: Salt; Cloned unidirectionally;
clone at primed. Average insert size 1.769 kb. Library
enriched for full length clones and constructed by Life
Technologies. Note: this is a NIH_MGC library."
1 others
BASE COUNT 163 a 493 c 244 g 210 t
ORIGIN
Query Match 57.3% Score 362.4; DB 14; Length 1061;
Best Local Similarity 77.7% Pred. No. 1,40-84;
Matches 508; Conservative 0; Mismatches 101; Indels 45; Gaps 4;
12 GTCCACACACAGTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGGACATAT 71
139 GTCCACACAGTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGGACATAT 198
72 GTCCACACAGTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGGACATAT 131
199 GTCCACACAGTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGGACATAT 258
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252 TGACACAGTGTGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 299
376 TGACACAGTGTGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 435
300 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 359
436 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 495
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496 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 555
415 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 452
556 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 615
453 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 512
616 TGATATCATCAGTATGCTGGGAGTATGCTTTGGTTTTCACCACTCGGGTGGATGGG 675



GenCore version 5.1.1
Copyright (c) 1993 - 2002 Compugen Ltd.
OR database nucleic acid, using seq.mage
Run on: December 29, 2002, 09:34:31, Batch time 52 Seconds
(without alignments)
3733,200 Million cell updates/sec
Title: US-09-727-770-1
Perfect score: 633
Seq-09-727-770-1
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 441362 seqs, 15338481 residues

Total number of hits satisfying chosen parameters: 982724

Minimum hit seq length: 0
Maximum hit seq length: 20000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	47.2	5.9	1344	1	US 08 705 771 8 Sequence 8, Appl
3	45.6	5.6	7218	1	US 08 232 453 14 Sequence 14, Appl
4	44.8	5.5	2243	3	US 09 084 079 4 Sequence 4, Appl
5	44.4	5.4	2485	1	US 08 424 424 1 Sequence 1, Appl
6	44.4	5.4	2496	2	US 09 094 647 1 Sequence 1, Appl
7	44.4	5.4	2919	4	US 09 409 647 1 Sequence 1, Appl
8	43.8	5.3	2735	1	US 08 698 551 11 Sequence 11, Appl
9	43.8	5.3	2735	2	US 08 692 229 11 Sequence 11, Appl
10	43.8	5.3	2735	2	US 08 494 440 11 Sequence 11, Appl
11	43.8	5.3	2735	2	US 08 533 901 11 Sequence 11, Appl
12	43.8	5.3	2735	2	US 08 839 032 11 Sequence 11, Appl
13	43.8	5.3	2735	2	US 08 839 032 11 Sequence 11, Appl
14	43.8	5.3	2735	2	US 08 839 032 11 Sequence 11, Appl
15	43.8	5.3	2735	2	US 08 839 032 11 Sequence 11, Appl
16	43.8	5.3	2735	2	US 08 839 032 11 Sequence 11, Appl
17	43.8	5.3	6002	2	US 08 698 551 15 Sequence 15, Appl
18	43.8	5.3	6002	2	US 08 698 551 15 Sequence 15, Appl
19	43.8	5.3	6002	2	US 08 698 551 15 Sequence 15, Appl
20	43.6	5.3	50341	1	US 09 185 2580 15 Sequence 15, Appl
21	43.6	5.3	50341	2	US 09 247 901 11 Sequence 1, Appl
22	43.6	5.3	50341	2	US 09 075 904 11 Sequence 1, Appl
23	43.4	5.3	52297	4	US 09 426 436 1 Sequence 1, Appl
24	43.4	5.3	52297	4	US 08 705 557 1 Sequence 1, Appl
25	43.4	5.3	2556	3	US 08 699 1038 9 Sequence 9, Appl
26	43.4	5.3	2731	4	US 09 229 059 11 Sequence 11, Appl
27	43.4	5.3	2731	4	US 09 229 059 11 Sequence 11, Appl

28	33.2	5.2	1801	1	US 08 557 917A 1 Sequence 1, Appl
29	32.2	5.2	1801	2	US 08 557 917A 1 Sequence 1, Appl
30	32.2	5.2	1801	3	US 08 557 917A 1 Sequence 1, Appl
31	32.6	5.2	960	4	US 09 576 160 10 Sequence 10, Appl
32	32.6	5.2	1053	4	US 09 576 160 11 Sequence 11, Appl
33	32.4	5.1	2061	4	US 09 310 463 21 Sequence 21, Appl
34	32.4	5.1	2061	4	US 08 842 249A 22 Sequence 22, Appl
35	32.4	5.1	2123	1	US 08 163 343A 3 Sequence 3, Appl
36	32.4	5.1	2483	5	US 08 594 084 9A 3 Sequence 3, Appl
37	32.2	5.1	946	4	US 09 543 597 118 Sequence 118, Appl
38	32.2	5.1	1896	4	US 09 345 468 24 Sequence 24, Appl
39	32.2	5.1	1896	4	US 09 414 453A 24 Sequence 24, Appl
40	32.2	5.1	2170	4	US 09 445 468 11 Sequence 11, Appl
41	32.2	5.1	2170	4	US 09 445 468 11 Sequence 11, Appl
42	32.2	5.1	2194	4	US 09 310 463 19 Sequence 19, Appl
43	32.2	5.1	2194	4	US 08 842 249A 19 Sequence 19, Appl
44	32.2	5.1	18596	4	US 09 318 448 11 Sequence 11, Appl
45	31.8	5.0	3024	1	US 08 149 100 1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US 08 807-044-2
Sequence 2, Application US/08807044
Patent No. 5863745
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN TRANSMEMBRANE 4 SUPERFAMILY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: 12755 Pharmaceuticals, Inc.
STREET: 12755 Pharmaceuticals, Inc.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,044
FILING DATE: Retewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/BACKUP NUMBER: FF 0224 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SCORNOT01
CLONE: 663655
US 08 807 044 2

Query Match 6.1%, Score 38.8, UB 2; Length 1151;
Best Local Similarity 51.1%, Pred. No. 0.046, 87; indels 0; Gaps 0;
Matches 91, Conservative 0, Mismatches 87

QY 537 ACTAGTATCTTCAAGTATACACTGCTCTCTGTTCATGCTGCTGTCAGAGAGCTTG 596
 DB 1346 YY 1405
 QY 597 GCGGTGCG 632
 DB 1406 YY 1441

RESULT 4

US-09-084-079-4
 ? Sequence 4, Application US/0904079
 ? Patent No. 6150146
 ? GENERAL INFORMATION
 ? APPLICANT: Bronstein, Jeff M.
 ? APPLICANT: Soitz, Robert S.
 ? APPLICANT: Tallone, Roger L.
 ? TITLE OF INVENTION: High-Speed Poly-Seq-110 P: Data and Method for
 ? TITLE OF INVENTION: Diagnosing and Treating Disease
 ? NUMBER OF SEQUENCES: 5
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Sheldon S. Mui
 ? STREET: 220 S. Lake Avenue, 9th Floor
 ? CITY: Pasadena
 ? STATE: California
 ? ZIP: 91101

? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 ? COMPUTER: IBM compatible
 ? OPERATING SYSTEM: Windows 95
 ? SOFTWARE: WordPerfect for Windows version 8.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US-09-084-079
 ? FILING DATE: 22 MAY 1998
 ? CLASSIFICATION:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Farah, David A.
 ? REGISTRATION NUMBER: 38134
 ? REFERENCE/DOCKET NUMBER: 11201-1
 ? TELEPHONE: (626)796-4000
 ? TELEFAX: (626)795-6241
 ? INFORMATION FOR SEQ ID NO: 4:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 2443 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: cDNA to mRNA
 US-09-084-079-4

Query Match 5.54; Score 34.8; DB 1; Length 2443
 Best Local Similarity 52.0%; Pred. No. 0.99; Indels 0; Gaps 0;
 Matches 78; Conservative 0; Mismatches 72
 QY 44 TCAATCATCTGGGTGGTATAGGCACATAGCTCTCCAGTGGGTGGGTGGGTGGGCA 103
 DB 132 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 QY 104 TGGTAAAGATGGCAGCCGATATATGATATGATGATGATGATGATGATGATGAT 163
 DB 192 TGGTAAAGATGGCAGCCGATATATGATATGATGATGATGATGATGATGATGAT 251
 QY 164 TGAATTCATCATCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 194
 DB 252 TGAATTCATCATCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 281

RESULT 5

US-09-424-424B-1
 ? Sequence 1 Application US/09424424B
 ? Patent No. 5759854

? GENERAL INFORMATION:
 ? APPLICANT: LI, ET AL.
 ? TITLE OF INVENTION: Neurotransmitter Transporter
 ? NUMBER OF SEQUENCES: 6
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: CARELLA, BYRNE, RAIN, GILFILLAN,
 ? ADDRESSEE: CECCHI, STEWART & OLSTEIN
 ? STREET: 6 BECKER FARM ROAD
 ? CITY: ROSELAND
 ? STATE: NEW JERSEY
 ? COUNTRY: USA
 ? ZIP: 07068
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5 INCH DISKETTE
 ? COMPUTER: IBM PS/2
 ? OPERATING SYSTEM: MS-DOS
 ? SOFTWARE: WORD PERFECT 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US-09-424-424B
 ? FILING DATE: APRIL 21, 1995
 ? CLASSIFICATION: 435
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: PCT/US94/05364
 ? FILING DATE: MAY 25, 1996
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: MULLINS, J.G.
 ? REGISTRATION NUMBER: 33,073
 ? REFERENCE/DOCKET NUMBER: 325800-308
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 201-994-1700
 ? TELEFAX: 201-994-1744
 ? INFORMATION FOR SEQ ID NO: 1:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 2485 BASE PAIRS
 ? TYPE: NUCLEIC ACID
 ? STRANDEDNESS: SINGLE
 ? TOPOLOGY: LINEAR
 ? MOLECULE TYPE: cDNA
 US-09-424-424B-1

Query Match 5.48; Score 34.4; DB 1; Length 2485;

Best Local Similarity 46.3%; Pred. No. 1.4;
Matches 113; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

QY 8 ACATGTCACCAACACAGCCCGAGATAGCTTTGCTTTTTCACCAATCTGCGGTGCTATGCCCA 57
 DB 1113 ACAATGTCACCTCCAGTCCAGTGGGACACATCTGACACCCCGAGTGTCTGCGGAGGATACCA 1172
 QY 68 CCAATGCTCCAGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 127
 DB 1173 CCAATGCTCCAGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1242
 QY 126 TGGTAT 137
 DB 1234 ATATAC 1292
 QY 188 TGGTGGTATCATCATCCATATGCGGTAGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 247
 DB 1294 CCAATGCTCCAGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1352
 QY 248 ATCA 251
 DB 1353 ATCA 1356

RESULT 6

PCT-US94-05364A-1
 ? Sequence 1, Application PCT/US9405364A
 ? GENERAL INFORMATION:
 ? APPLICANT: LI, ET AL.
 ? TITLE OF INVENTION: Neurotransmitter Transporter
 ? NUMBER OF SEQUENCES: 2
 ? CORRESPONDENCE ADDRESS:

Tue Dec 31 14:03:11 2002

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ADDRESSEE: CECCHI, STEWART & OLSTEIN
 STREET: 6, BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05363A
 FILING DATE: SUBMITTED HERewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: FERRARO, GREGORY D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 425800-118
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2494 BASE PAIRS
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: cDNA
 PCT-US94-05363A-1

Query Match: 5.4%; Score 34.4; DB 5; Length 2486;
 Best Local Similarity 46.3%; Pred. No. 1.4;
 Matches 131; Conservative 0; Mismatches 131; Indels 0; Gaps 0;
 QY 8 ACATCTCCCAACACACCGCGGACTATGCTTTCTTTTTCACATCTCGGCTGCTATGCGCA 67
 DB 1114 ATATTTTTCATCCCAACAGTGGTCAATGCTGACCGCGGAGTGTGCGGAGTAGCTA 1173
 QY 68 CCAAGTCTCCAGTGGGCTGGGCTGGCTGTGGCATGGCCAGAAATGGACCGGATCA 127
 DB 1111 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 DB 1174 CACAGGCTCTTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1233
 QY 128 TGGCAATGCTGTGTCATGTGGCCAGAGCTGAACACATGAAGTGCATCGCATCGGATCA 187
 DB 1234 ATAGAGAGACACACACTGCGCATTGATATGATGATGATGATGATGATGATGATGATGAT 1293
 QY 188 TGGTGGTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 247
 DB 1294 CCGTACGTTGGCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1453
 QY 248 ATCA 251
 DB 1354 ATCA 1357

RESULT 7
 US-09-408-647A-1
 Sequence 11, Application US/09408647A
 Patent No. 6499858
 GENERAL INFORMATION:
 APPLICANT: Kobayashi, Donald
 TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas
 FILE OF INVENTION: maltophilia
 FILE REFERENCE: PCT-US94-05363A
 CURRENT APPLICATION NUMBER: US/09/408,647A
 CURRENT FILING DATE: 1999-08-26
 PRIOR APPLICATION NUMBER: 60/098,046
 PRIOR FILING DATE: 1998-08-27

NUMBER OF SEQ ID NOS: 2
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 2810
 TYPE: DNA
 ORGANISM: Stenotrophomonas maltophilia
 FEATURES:
 NAME/KEY: CDS
 LOCATION: (306)...(2405)
 OTHER INFORMATION: open reading frame 1 (ORF1)
 NAME/KEY: sig_peptide
 LOCATION: (306)...(428)
 NAME/KEY: terminator
 LOCATION: (2457)...(2481)
 NAME/KEY: 5HS
 LOCATION: (295)...(298)
 NAME/KEY: CDS
 LOCATION: (314)...(2162)
 OTHER INFORMATION: open reading frame 2 (ORF2)
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: Genbank No. 6499858 AF014950
 DATABASE ENTRY DATE: 1997-09-23
 US-09-408-647A-1

Query Match: 5.4%; Score 34.4; DB 4; Length 2810;
 Best Local Similarity 44.9%; Pred. No. 1.5;
 Matches 131; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
 QY 8 ACATCTCCCAACACACCGCGGACTATGCTTTCTTTTTCACATCTCGGCTGCTATGCGCA 67
 DB 1747 ACACCGCCCAACTACACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1806
 QY 68 CCAAGTCTCCAGTGGGCTGGGCTGGCTGTGGCATGGCCAGAAATGGACCGGATCA 127
 DB 1807 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1866
 QY 128 TGGCAATGCTGTGTCATGTGGCCAGAGCTGAACACATGAAGTGCATCGCATCGGATCA 187
 DB 1867 CCGGCGGCTGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1926
 QY 188 TGGTGGTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 247
 DB 1927 CCGTGGGATCGCGAGACACACATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1986
 QY 248 ATGATCACACACTGCTCTATAGCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 299
 DB 1987 CCGGCGGACCAAGCTCTACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2048

RESULT 8
 US-08-698-551-11
 Sequence 11, Application US/08698551
 Patent No. 5712481
 GENERAL INFORMATION:
 APPLICANT: Lilo, Lih-Ling
 APPLICANT: Chen, Jennifer H.
 APPLICANT: Schiavella, Andrea
 APPLICANT: Graham, James
 TITLE OF INVENTION: NOVEL INF PEPTIDE DEATH D-MAIN LIGAND
 TITLE OF INVENTION: PROTEINS AND INHIBITORS OF LIGAND BINDING
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genetics Institute, Inc.
 STREET: 87 Cambridgepark drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25


```

1 RESULT 11
2 US-08-533-901B-11
3 : Sequence 11, Application US/08533901B
4 : Patent No. 5852173
5 : GENERAL INFORMATION:
6 : APPLICANT: Lin, Lih-ling
7 : APPLICANT: Chen, Jennifer H.
8 : APPLICANT: Schiavello, Andrea
9 : APPLICANT: Graham, James
10 : TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND
11 : TITLE OF INVENTION: PROTEINS AND INHIBITORS OF LIGAND BINDING
12 : NUMBER OF SEQUENCES: 15
13 : CORRESPONDENCE ADDRESS:
14 : ADDRESSEE: Genetics Institute, Inc.
15 : STREET: 87 Cambridgepark Drive
16 : CITY: Cambridge
17 : STATE: Massachusetts
18 : COUNTRY: USA
19 : ZIP: 02140
20 : COMPUTER PLATFORM: P486.
21 : MEDIUM TYPE: Floppy disk
22 : COMPUTER: IBM PC compatible
23 : OPERATING SYSTEM: PC-DOS/MS-DOS
24 : SOFTWARE: Patent In Release #1.0, Version #1.25
25 : CURRENT APPLICATION DATA:
26 : ATTORNEY NAME: B. BIRNBERG US 690 632 0010
27 : FILING DATE:
28 : CLASSIFICATION: 435
29 : ATTORNEY/AGENT INFORMATION:
30 : NAME: BROWN, Scott A.
31 : REGISTRATION NUMBER: 32,724
32 : REFERENCE/DOCKET NUMBER: G15232
33 : TELECOMMUNICATION INFORMATION:
34 : TELEPHONE: (617) 498-8224
35 : TELEFAX: (617) 876-5851
36 : INFORMATION FOR SEQ ID NO. 11:
37 : SEQUENCE CHARACTERISTICS:

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Tue Dec 31 14:03:11 2002

us-09-727-770-1.rni

Db 222 C 222

Search completed: December 28, 2002, 10:57:07

Job time : 62 secs

Db 162 AUGGAGAGAGAGTCCACACGAAAGGAGAAATGAGGAGTGGGAGGATGCTGGGCTAG 221

QY 420 C 420

Db 222 C 222

RESULT 15

PCT-US95-12724-11

: Sequence 11, Application PC/TUS9512724

: GENERAL INFORMATION:

: APPLICANT: Lin, Lih-Ling

: APPLICANT: Chen, Jennifer H.

: APPLICANT: Schiavella, Andrea

: APPLICANT: Graham, James

: TITLE OF INVENTION: NOVEL TRP RECEPTOR DEATH DOMAIN LIGAND

: TITLE OF INVENTION: PROTEINS AND INHIBITORS OF LIGAND BINDING

: NUMBER OF SEQUENCES: 14

: CORRESPONDENCE ADDRESS:

: ADDRESS: Genetics Institute, Inc.

: STREET: 87 Cambridgepark Drive

: CITY: Cambridge

: STATE: Massachusetts

: COUNTRY: USA

: ZIP: 02140

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: PC/TUS95/12724

: FILING DATE:

: CLASSIFICATION:

: ATTORNEY/AGENT INFORMATION:

: NAME: BLOOM, SCOTT A.

: REGISTRATION NUMBER: 32,724

: REFERENCE/AGENT NUMBER: 3152128

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (617) 498-8224

: TELEFAX: (617) 876-5851

: INFORMATION FOR SEQ ID NO: 11:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 2745 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: double

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA

: HYPOTHETICAL: NO

: FEATURE:

: NAME/KEY: CDS

: LOCATION: 2..1922

: PCP-US95-12724-11

Query Match 5.38; Score 33.8; DB 5; Length 2735;

Best local Similarity 49.28; Pred. No. 2.2;

Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 140 TCATGTCGTCAGAGTCAATCCACATGAAGTCAATCATGTCAGTGGTGGTATCA 199

Db 42 TCAGGTGATGAGTCCCTCAGCTTGACACAGAGCTCTATGCCACAGCGGCTCTGGGTGGATGG 101

QY 200 TCACCATCATGCGCTAGTGGGCGCTGTGCGCGCAACTGCGCTGAAATGATGACAACA 259

Db 102 CCAGCATCTTTGGGCTTTTGGAGATTGCCAGAGCCCACTACTATAGTAAAGAACACAGACA 161

QY 260 GTCTCTATACACATTTCTGTCACAGCTGGGCGTGGCTGAGTGGGCTGGGAGCGCGGCTTG 319

Db 162 AGCGAAGAGAGAGTCCGAAACAGAAAGGTAAATACCCAGCTTGGCAAGCACTCTGGCTAG 221

QY 420 C 420


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QY 1 MetSerAspAsnSerProGlnThrAlaValAlaPheThrThrSerGlyAlaValAlaValMet 20
|||||
Db 106400 AIGTCACAAACAGCCCGAGTAGTGTGGTTTTCACCATCTCCGGTGTCTATGGCCACC 106441
CQ 22 M-Val202SerGlyLeuThrAlaAlaCysGlyMetValAlaCysAsnGlyThrThrThrMet 46
|||||
Db 106440 AIGTCCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 106481
CQ 41 AlMetSerValMetIlePheGlnLeuIleHisMetIleSerGlyThrIleValValMet 60
|||||
Db 106780 GTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 106721
CQ 61 AlMetIleIleThrIleThrIleValAlaAlaValIleThrAlaAlaSerIleValMet 80
|||||
Db 106720 GCTGGTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 106661
CQ 81 AsnAlaPheSerLeuThrSerProSerProSerProSerProSerProSerProSerPro 100
|||||
Db 106660 GAGCAACAGAGTCTCTATAGACAGTTCCTGTCACATGCTGCTGCTGCTGCTGCTGCTG 106601
QY 101 AlAlaGlyPheAlaIleValIleValAlaGlyAspThrGlyLysCysGlyThrAlaGlnGlnPro 120
|||||
Db 106600 GAGAGTTTGCCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 106541
QY 121 ArgLeuPheValGlyMetIleLeuIleLeuIlePheAlaAlaValIleValIleLeuSerThr 140
|||||
Db 106540 GAACTATTGTAGACATGATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 106481
QY 141 LysGlnProLeuSerLysProThrThrHisAlaValIleAlaCysGlyAspHisProSerSer 160
|||||
Db 106480 AAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 106421
QY 161 PheAlaGlnSerProSerProSerProSerProSerProSerProSerProSerProSer 180
|||||
Db 106420 TTCCGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 106361
QY 181 LeuSerValGlnCysProArgValHisArgLeuLeuAlaArgProCysProLeuProPro 200
|||||
Db 106360 CTAAAGTACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 106301
QY 201 HisAlaValAlaAspIle 205
|||||
Db 106300 CAIGCTGTGTAATC 106246

RESULT 4
AC015913
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

```

TITLE JOURNAL

REFERENCE AUTHORS

Testaye, S., Tittel, A., Vassiliev, B., Wu, X., Wheeler, J., Wu, X., Wymann, D., Ye, W.J., Zimmer, A., and Zody, M.
Direct Submission
Submitted (17-Nov-1999) Whitehead Institute/MIT Center for Genome Research, 420 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 184595)
Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, R., Bastien, V., Bloom, J., Boguslavsky, L., Boukhvalter, B., Camarillo, J., Chang, J., Chazotte, G., Chazotte, Y., Collymore, A., Cook, A., Cooke, P., DeArenillas, K., Dewar, K., Diaz, J.S., Dodge, S., Farris, S., Ferreira, P., Fitzgerald, M., Gage, D., Galadon, J., Gardina, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, R., Hattori, I., Holmes, W., Ilavsky, J., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, S., MacLean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneses, L., Mihova, T., Miska, V., Murphy, T., Nayler, J., Naylor, J., O'Neill, D., Oliver, J., Peterson, K., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phipps, P., Pierre, N., Raymond, C., Petia, P., Pise, C., Porco, P., Roman, J., Roy, A., Schaefer, S., Schack, P., Seaman, S., Seery, P., Smith, C., Spencer, B., Stange, Thomas, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Totham, K., Travers, M., Vassiliev, B., Viel, R., Vo, A., Wilson, B., Wu, X., Wymann, D., Young, G., Zaimoun, J., Zembek, L., Zimmer, A., and Zody, M.
Direct Submission
Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 420 Charles Street, Cambridge, MA 02141, USA
On Oct. 27, 2001 this sequence version replaced gi:16356913.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
<http://www.sanger.ac.uk/Software/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
<http://www.wibrr.com>
Contact: Sequence Submissions: genome.wi.mit.edu
----- Project Information
Center project name: BLA22
Center clone name: BLA22
----- Summary Statistics
Sequencing vector: ML3; M77815; 40% of reads
Sequencing method: Plasmid; 60%; 60% of reads
Chemistry: Dye primer; 2% of reads
Assembly program: Phrap; version 0.960741
Consensus quality: 168221 bases at least Q40
Consensus quality: 175550 bases at least Q30
Consensus quality: 172768 bases at least Q20
Insert size: 203600; agarose-1p
Quality score: 181495; sum-of-contigs
Quality coverage: 7.6 in Q20 bases.
* NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

TITLE JOURNAL

REFERENCE AUTHORS

10664 10763: gap of 100 bp
10764 11392: contig of 629 bp in length
11393 11492: gap of 100 bp
11493 12333: contig of 841 bp in length
12334 12433: gap of 100 bp
12434 13332: contig of 899 bp in length
13333 13432: gap of 100 bp
13433 14716: contig of 1284 bp in length
14717 14816: gap of 100 bp
14817 16181: contig of 1285 bp in length
16182 16201: gap of 100 bp
16202 17797: contig of 1596 bp in length
17798 17897: gap of 100 bp

[illegible]

[illegible]

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.27% Matches: 2
DB: 3 Gaps: 0

US 09-727-770-2 (1-205) x DMSDR0 (1-7252)

QY 115 GlyThrAlaGlnGlnProArgGluAlaValGlyMetIleIleuIleuIlePheAla 133
|||||
DB 6600 GGCACAGACACAGCAGCAGTATGCTGCTGGGATGATGCTATCTCACTCTGGCC 6656
|||||

RESULT 42
AC013221
LOCUS AC013221 10813 bp DNA linear HTG 07-Sep-2001
DEFINITION Mus musculus mvp gene for vacuolar H⁺-ATPase 16 kDa proteolipid subunit, complete cds.
ACCESSION AB059462
VERSION AB059462.1 GI:15437404
KEYWORDS
SOURCE
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Hayami,K., Noumi,T., Inoue,H., San-Mada,G., Yoshimizu,T. and Kanazawa,H.
TITLE The murine genome contains one functional gene and two pseudogenes coding for the 16 kDa proteolipid subunit of vacuolar H⁺-ATPase
JOURNAL Gene 273 (2): 199-206 (2002)
MEDLINE 21479304
REFERENCE 2
AUTHORS Hanada,H., Hasche,M., Moriyami,Y., Mardin,M. and Futai,M.
TITLE Molecular cloning of cDNA encoding the 16 kDa subunit of vacuolar H⁺-ATPase from mouse cerebellum
JOURNAL Biochem. Biophys. Res. Commun. 176 (1): 1062-1067 (1991)
MEDLINE 91428192

ALIGNMENT Scores:
Pred. No.: 2,510-08 Length: 10813
Score: 19,000 Matches: 19
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.27% Indels: 0
DB: 10 Gaps: 0

US 09-727-770-2 (1-205) x AB059462 (1-10813)

QY 115 GlyThrAlaGlnGlnProArgGluAlaValGlyMetIleIleuIleuIlePheAla 133
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DB 9026 GGCACAGACACAGCAGCAGTATGCTGCTGGGATGATGCTATCTCACTCTGGCC 9082
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RESULT 42
AC013221
LOCUS AC013221 23870 bp DNA linear HTG 03-Nov-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
ACCESSION AC013221
VERSION AC013221.1 GI:6223111
KEYWORDS HTG: HTGS, PHASE2.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
REFERENCE 1
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (09-Nov-1999) Celera Genomics, 45 West Gate Drive, Rockville, MD, USA
COMMENT This sequence was identified as GDM1021307 by the submitter. For further information on this sequence you may e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

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location/Qualifiers
1..23870
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

BASE COUNT 6932 a 4966 c 4832 g 7140 t
ORIGIN

Alignment Scores:
Pred. No.: 4,424-96 Length: 23870
Score: 19,000 Matches: 19
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.27% Indels: 0
DB: 2 Gaps: 0

US 09-727-770-2 (1-205) x AB059462 (1-10813)

QY 115 GlyThrAlaGlnGlnProArgGluAlaValGlyMetIleIleuIleuIlePheAla 133
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DB 15968 GGCACAGACACAGCAGCAGTATGCTGCTGGGATGATGCTATCTCACTCTGGCC 15964
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RESULT 33
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LOCUS AC018035 41809 bp DNA linear HTG 09-Nov-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
ACCESSION AC018035
VERSION AC018035.1 GI:6554155
KEYWORDS HTG: HTGS, PHASE2.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
REFERENCE 1
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (09-Nov-1999) Celera Genomics, 45 West Gate Drive, Rockville, MD, USA
COMMENT This sequence was identified as GDM1021307 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced

5. (Basos 1 to 335026)
 Lewis, S.E.
 Direct Submission
 Submitted (31-MAY-2022) University of California Berkeley, 539 Life
 Sciences Addition, Berkeley, CA 94720, USA
 On Jun 28, 2022 this sequence version replaced 41:10727129
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 159327..164022

JOURNAL Chem. 272 (35), 2497-2498 (1997)
 MEDLINE 97450964
 REFERENCE 2 (bases 1 to 983)
 AUTHORS Oka.T.
 JOURNAL Direct Submission
 TITLE Submitted (04 FEB 1997) to GenBank, U.S.A. National Library of
 Institute of Scientific and Industrial Research, 8-1 Mihodaka,
 Ibaraki, 305-8565, Japan (P. O. Box 133, Tsukuba, Ibaraki 305-8565, Japan).
 Tel: 81-6-879-8491, Fax: 81-6-875-5724

FEATURES
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 /db_xref "taxon:6239"
 24..509
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 Prod. No.: 4,376-08 Length: 983
 Score: 18.00 Matches: 18
 Percent Similarity: 100.00% Conservat: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.78% Indels: 0
 DB: 3 Gaps: 0

US 09-727-770-2 (1-205) x AB000918 (1-983)
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JOURNAL Chem. 272 (35), 2497-2498 (1997)
 MEDLINE 97450964
 REFERENCE 2 (bases 1 to 983)
 AUTHORS Oka.T.
 JOURNAL Direct Submission
 TITLE Submitted (04 FEB 1997) to GenBank, U.S.A. National Library of
 Institute of Scientific and Industrial Research, 8-1 Mihodaka,
 Ibaraki, 305-8565, Japan (P. O. Box 133, Tsukuba, Ibaraki 305-8565, Japan).
 Tel: 81-6-879-8491, Fax: 81-6-875-5724

FEATURES
 source Location/Qualifiers

1..983
 /contig "Caenorhabditis elegans"
 /db_xref "taxon:6239"
 24..509
 /codon_start -1
 /product "VHA-2"
 /protein_id "AA022596.1"
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Alignment Scores:
 Prod. No.: 4,376-08 Length: 983
 Score: 18.00 Matches: 18
 Percent Similarity: 100.00% Conservat: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.78% Indels: 0
 DB: 3 Gaps: 0

US 09-727-770-2 (1-205) x AB000918 (1-983)
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/notes for a graphical representation of this gene seq.
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gene

Alignment Scores:

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Score: 18,00 Matches: 18
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8,78% Indels: 0
DB: 3 Gaps: 0

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US-09-727-770-2 (1-205) x AC024762 (1-49705)

Q7 115 HyThraAlaGlnProAlaLeuPheValGlyMetIleLeuIleLeuIlePhe 142

DB 24040 GGAACCTCAACACGACGCTTTTCGTGAGGAATGATCTTATCTTATCTTIC 22987

RESULT 50

AC006745

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DEFINITION AC006745 249287 bp DNA linear HTG 24-FEB-1999
Caenorhabditis elegans clone Y38F2. *** SEQUENCING IN PROGRESS ***
5 unordered pieces.

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AC006745

AC006745.1 GI:4263193

HTG: HTGS_PHASE1

Caenorhabditis elegans.

Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditidae; Rhabditidae; Telodoridae; Caenorhabditis.

1 (bases 1 to 249287)

Waterston,R.H.

The sequence of Caenorhabditis elegans clone

Unpublished

2 (bases 1 to 249287)

Waterston,R.H.

Direct Submission

Submitted (24-FEB-1999) Genome Sequencing Center, Washington

University School of Medicine, 444 Forest Park Parkway, St. Louis,

MO 63108, USA

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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* 1 147084: contig of 147084 bp in length
* 147085 147093: gap of unknown length
* 147094 187319: contig of 40226 bp in length
* 187320 187328: gap of unknown length
* 187329 189480: contig of 2152 bp in length
* 189481 189489: gap of unknown length
* 189490 245636: contig of 56147 bp in length
* 245637 245644: gap of unknown length
* 245645 249287: contig of 3643 bp in length.

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COMMENT:

FEATURES

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Source: 1. 249287
Organism: "Caenorhabditis elegans"
Accession: "F00053.239"
Clone: "Y38F2"

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BASE COUNT 79273 a 44143 c 43858 g 80582 t 1431 others
ORIGIN

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Alignment Scores:

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Pred. No.: 2,280-06 Length: 249287
Score: 18,00 Matches: 18
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DB: 2 Gaps: 0

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US-09 727 770 2 (1 205) x AC006745 (1 249287)

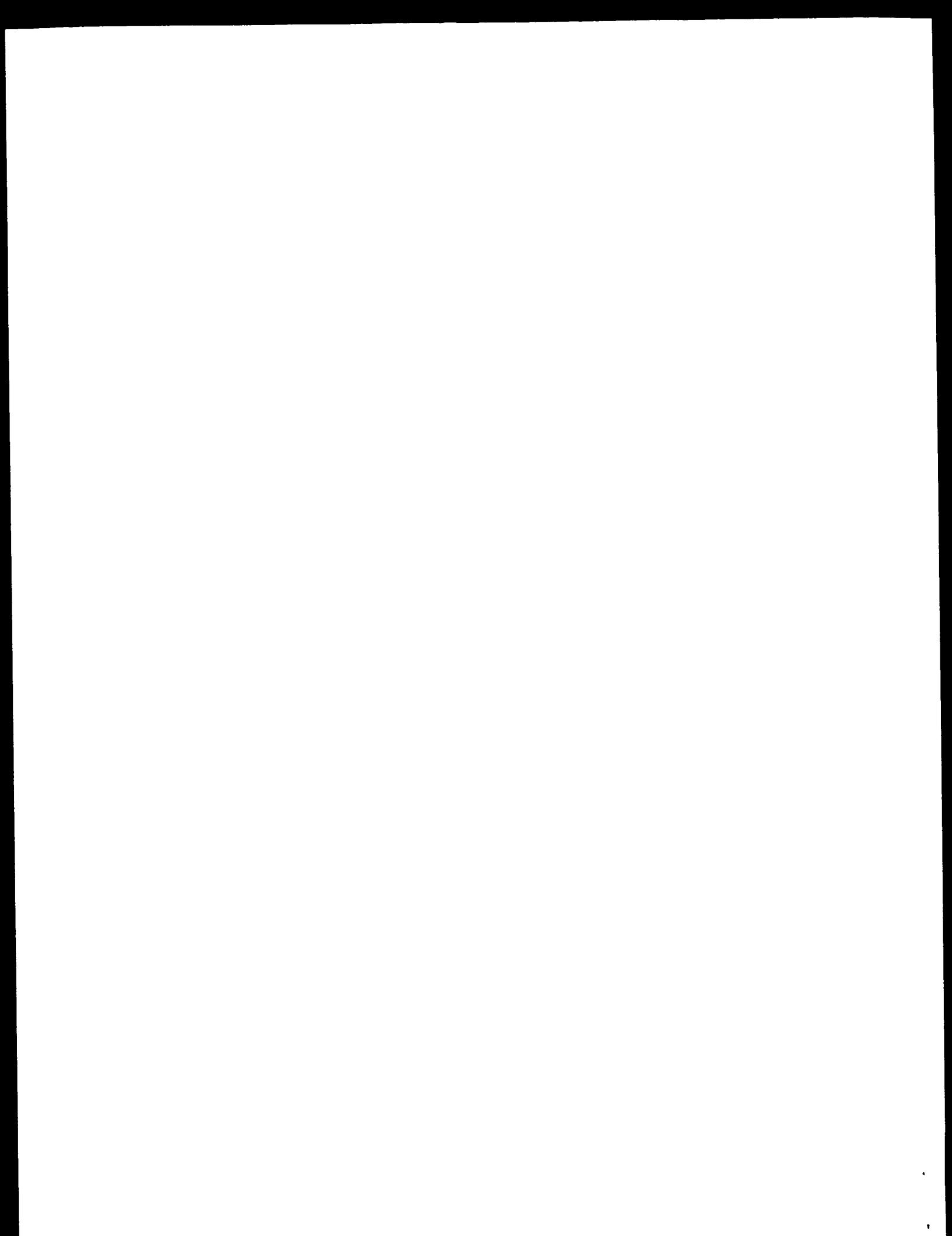
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DB 50918 GGAACGCTCAACACGACGCTTTTCGTGAGGAATGATCTTATCTTATCTTIC 50971

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Search completed: September 28, 2002, 14:17:41
Job time : 3053 secs

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PI /standard_name= "Single nucleotide polymorphism"
 XX W-200194380-A2.
 XX 13-DEC-2001.
 XX 41-MAY-2001; 2001WO-0517511.
 XX 02-JUN-2000; 2000US-208836P.
 XX 04-DEC-2000; 2000US-0727770.
 XX (APPL-) APPLERA CORP.
 XX Li Z, Wei M, Fretwell P, Borelby JM.
 XX WPI: 2002 566438/60.
 XX P-PSDB: AAO19455.
 XX New human transporter proteins related to the proton ATPase transporter
 PI: substantially for diagnosing and treating diseases mediated by the
 PI transporter protein and for identifying modulators
 XX Claim 23: Fig 3: 70pp; English.
 XX The invention comprises the amino acid and coding sequence of a human
 CC transporter protein, transporter proteins regulate many different
 CC functions of a cell, including cell proliferation, differentiation and
 CC signalling processes. Transporter proteins function by regulating the
 CC flow of molecules such as ions and macromolecules into and out of cells.
 CC The gene for the human transporter protein is located on chromosome 17.
 CC The DNA and protein sequences of the invention are useful for identifying
 CC agents that modulate or bind to the human transporter protein. The DNA
 CC and protein sequences are useful for treating a disease or condition that
 CC is mediated by a human transporter protein. The DNA and protein sequences
 CC of the invention may also be used in the construction of transgenic
 CC animals, pharmacogenomic analysis and for tissue typing. The present DNA
 CC sequence encodes the human transporter protein of the invention.
 XX Sequence 6339 BP: 1613 A; 1626 C; 1609 G; 1491 T; 0 other;
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 Alignment Scores:
 Pred. No.: 1,90-196 Length: 6,439
 Score: 205.00 Matches: 205
 Percent Similarity: 100.00% Conservat: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 DB 3000 ATGTCCAAACACAGCCGAGATATGTTTTCACATATCTGGATGTAAGGTAAC 3059
 QY 21 MetValSerSerClyLeuGlyAlaAlaCysGlyMetAlaLysAsnGlyThrGlyIleMet 40
 DB 3060 ATGGTCTCAGTGGGCTGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3119
 QY 41 AlaMetSerValMetIleProGlyLeuIleHisMetLysSerIleIleProValValMet 60
 DB 3126 GTCATGCTGTCATGTCGTCACAGTGTGATGATGATGATGATGATGATGATGATGATG 3179
 QY 41 AlaGlyThrIleThrIleThrIleThrIleThrIleThrIleThrIleThrIleThrIle 80
 DB 3180 GTTGTATATCATGACCATATATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 3239
 QY 41 AspAspAsnSerLeuLysSerSerPheLeuIleLeuAlaValLeuProAlaLysThrAla 100
 DB 3240 GATGACACAGTCTATATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 3299
 QY 201 AlaGlyPheAlaIleValIleValIleValIleValIleValIleValIleValIleVal 120
 DB 3300 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3359

QY 121 ArgLeuPheValGlyMetIleLeuIleLeuIlePheValIleValIleLeuSerThr 140
 DB 3360 CGACTATTGTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3419
 QY 141 LysGlnProLeuSerLysProThrSerHisAspGlyIleLeuGlyLysAspHisProSerSer 160
 DB 3420 AAGCAGGCGCTCTCAAAACCCACAGTTCACAGATACGATGTAAGACACCCCTCTCTCA 3479
 QY 161 PheArgIleValLysGlnProAspThrHisValIleLeuGlyLysSerThrPheSerValIleValAspLeu 180
 DB 3480 TTTCGGCAACAACACAGCCCTGACACGATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 3539
 QY 181 LysSerValIleThrCysPheValIleHisAlaGlyIleAlaValIleValIleValIleVal 200
 DB 3540 CTAAGTGTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3599
 QY 201 HisAlaValAspIle 205
 DB 4600 CATGCTGTGACATC 4614
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 ID ARA46570
 XX
 AC ARA46570;
 XX
 CI C1 PUB 2002 (first entry)
 XX
 DE Human breast cell single exon nucleic acid probe #5265.
 XX
 KW Human; microarray; single exon probe; gene expression; breast;
 KW disease; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 IN W20015727: A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 10-JAN-2001; 2001WO-080662.
 XX
 PR 04-FEB-2000; 2000US-0190312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 10-JUN-2000; 2000US-0608408.
 PR 04-AUG-2000; 2000US-0632466.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236459.
 PR 04-OCT-2000; 2000GB-0021263.
 XX
 (MOLE) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI: 2001-496933/54.
 XX
 PT New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes
 XX
 PS Claim 4: SEQ ID NO 5265; 427pp + sequence listing; English.
 XX
 CC The invention relates to a spatially addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for
 CC determining predisposition and/or prognosis breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater

diversity of probes for measuring gene expression with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences.

Sequence 612 bp; 120 A; 195 C; 151 G; 146 T; 0 other;

Alignment Scores:
Pred. No.: 2,126-195 Length: 612
Score: 203.00 Matches: 203
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.02% Indels: 0
Gaps: 0

US-09-727-770-2 (1-205) x ABA64433 (1-612)

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QY 21 MetValSerGlyLeuValAlaValPheThrMetAlaValSerLeuMet 40
DB 63 ATGGTCTCCAGTGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 122
QY 41 AlaMetSerValMetTrpProGlnLeuIleHisMetLysSerIleIleProValValMet 60
DB 123 GCCATGCTGTCTGATGTCGCCACAGCGATGCCATGATGATGATGATGATGATG 182
QY 61 AlaGlyIleIleThrIleThrIleThrIleThrIleThrIleThrIleThrIle 80
DB 183 GCTGGTATCATCACCACATCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 242
QY 81 AspAspAsnSerLeuTyrSerSerPheLeuGlnLeuGlyAlaValSerGlyLeuAla 100
DB 243 GATGACACACAGTCTCATAGCAGTTCCTCCAGCTGGGCTGGGCTGGGCTGGG 302
QY 101 AlaGlyPheAlaIleValIleValIleValIleValIleValIleValIleValIle 120
DB 303 GCGGCGCTTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 362
QY 121 ArgPhePheValIleMetIleLeuIleLeuIlePheAlaValValIleLeuSerThr 140
DB 363 CCACATATTTCTAGGCATGATGATGATGATGATGATGATGATGATGATGATG 422
QY 141 LysGlnProLeuSerLysSerLysSerLysSerLysSerLysSerLysSerLys 160
DB 423 AAGCAGCGCTCTCAAAACCCACACACACACACACACACACACACACACACAC 482
QY 161 PheArAsnLysGlnProAspThrHisValLeuGlySerTrpProSerValValAspLeu 180
DB 483 TCCGGAACAAACAGCCCTGACACACACACACACACACACACACACACACAC 542
QY 181 LeuSerValGlnCysProArgValHisArdeuLeuLeuAlaArpProCysProLeuPro 200
DB 543 CTAAGTGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
QY 201 HisAlaVal 203
DB 603 CATGCTGTG 611

RESULT 4

ABA64433

ID ABA64433 standard: DNA: 612 bp.

XX

XX

XX 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #12748.

XX Human foetal liver gene expression: single exon nucleic acid probe: 88.
XX Homo sapiens.
XX W:290157277-A2.
XX 09 AUG-2001.
XX 10 JAN 2001: 2001W0-0500669.
XX 04-FEB-2000: 2000S-0180312.
XX 26-MAY-2000: 2000S-0207456.
XX 06-JUN-2000: 2000S-0608408.
XX 03-AUG-2000: 2000S-0632466.
XX 21-SEP-2000: 2000S-0234687.
XX 27-SEP-2000: 2000S-0246359.
XX 04-OCT-2000: 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Peim SG, Hanzel BK, Chen W, Bank BK
XX WPI: 2001-483447/52.
XX human genome derived single exon nucleic acid probes useful for
XX analyzing gene expression in human foetal liver
XX Claim 4: SEQ ID NO 12748: 639pp + sequence listing: English.
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at http://wipo.int/pub/published_pct_sequences.

Sequence 612 bp; 120 A; 195 C; 151 G; 146 T; 0 other;

Alignment Scores:
Pred. No.: 2,126-195 Length: 612
Score: 203.00 Matches: 203
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.02% Indels: 0
Gaps: 0

US-09-727-770-2 (1-205) x ABA64433 (1-612)

QY 1 MetSerAsnAsnSerLeuTyrAlaValPheThrIleSerGlyAlaMetAlaThr 20
DB 3 ATGTCCACACACACCCGAGTATGCTTGGTTCACATCTGGGTGCTATGCCACC 62
QY 21 MetValSerGlyLeuValAlaValPheThrMetAlaValSerLeuMet 40
DB 63 ATGGTCTCCAGTGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 122
QY 41 AlaMetSerValMetTrpProGlnLeuIleHisMetLysSerIleIleProValValMet 60
DB 123 GCCATGCTGTCTGATGTCGCCACAGCGATGCCATGATGATGATGATGATGATG 182
QY 61 AlaGlyIleIleThrIleThrIleThrIleThrIleThrIleThrIleThrIle 80
DB 183 GCTGGTATCATCACCACATCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 242
QY 81 AspAspAsnSerLeuTyrSerPheLeuGlnLeuGlyAlaValSerGlyLeuAla 100
DB 243 GATGACACACAGTCTCATAGCAGTTCCTCCAGCTGGGCTGGGCTGGGCTGGG 402
QY 101 AlaGlyPheAlaIleValIleValIleValIleValIleValIleValIleValIle 120

us-09-727-770-2.0110p2n.rng

Tue Dec 31 14:03:13 2002

XX OS Homo sapiens.
 XX PN W0200157275-A2.
 XX PD 09-AUG-2001.
 XX PR 30-JAN-2001; 2001W0-US00667.
 XX PR 04-FEB-2000; 2000US-0180412.
 XX PR 26-MAY-2000; 2000US-0207456.
 XX PR 30-JUN-2000; 2000US-0608408.
 XX PR 03-AUG-2000; 2000US-0632366.
 XX PR 21-SEP-2000; 2000US-0234687.
 XX PR 27-SEP-2000; 2000US-0246359.
 XX PR 04-OCT-2000; 2000GB-0024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX P1 Penn SG, Hanzel DK, Chen W, Rank DR;
 XX XX WPI; 2001 483446/52.
 XX PT Single exon nucleic acid probes for analyzing gene expression in human brains.
 XX PS Example 4; SEQ ID NO: 12882; 650pp + Sequence Listing, English.
 XX CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
 XX CC Sequence 612 BP; 120 A; 195 C; 151 G; 146 T; 0 other;
 XX SQ Alignment Scores:
 XX Pred. No.: 2,126-195
 XX Score: 203.00
 XX Percent Similarity: 100.00%
 XX Best Local Similarity: 100.00%
 XX Query Match: 99.02%
 XX Indels: 0
 XX Caps: 0
 XX DB: 22

DB 363 CGACTATTGTCAGGCAATGATGATGCTTGGTAAAGTGGTCACTCTCTGCA 422
 QY 141 TysGlnProLeuSerThrSerHisArgIleAlaGlyLysAspHisProSer 160
 DB 423 AAGCAAGCCCTCTCAAAACCCACACAGTCAAGATAATGATGTAAGACACCTCTCA 482
 QY 161 PheArgAsnLysGlnProAspThrHisValIleuGlySerTrpProSerValValAspLeu 180
 DB 483 TTGGGGAACAAACAGCTGACACGACATCTCTGAGTGGTCAAGTGGTGGTGGTGGTGG 542
 QY 181 LeuSerValGlnCysProArgValHisArgLeuLeuAlaAlaProCysProLeuProPro 200
 DB 543 CTAACTGTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
 QY 201 HisAlaVal 203
 DB 603 CATGCTGCTG 611
 RESULT 7
 AAK38619
 ID AAK38619 standard; DNA; 612 BP.
 AC XX
 DI XX
 DI 06-NOV-2001 (first entry)
 XX Human bone marrow expressed single exon probe SEQ ID NO: 14376.
 DE Human, bone marrow expressed exon; gene expression analysis; probe;
 KW metastasis; cancer; leukaemia; lymphoma; myeloma; ss.
 KW Homo sapiens.
 OS W0200157276-A2.
 PN 09-AUG-2001.
 PD 30-JAN-2001; 2001W0-US00668.
 XX PR 04-FEB-2000; 2000US-0180412.
 XX PR 26-MAY-2000; 2000US-0207456.
 XX PR 30-JUN-2000; 2000US-0608408.
 XX PR 03-AUG-2000; 2000US-0632366.
 XX PR 21-SEP-2000; 2000US-0234687.
 XX PR 27-SEP-2000; 2000US-0246359.
 XX PR 04-OCT-2000; 2000GB-0024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX P1 Penn SG, Hanzel DK, Chen W, Rank DR;
 XX XX WPI; 2001-488900/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
 XX PS Example 4; SEQ ID NO: 13176; 658pp + Sequence Listing, English.
 XX CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
 XX CC Sequence 612 BP; 120 A; 195 C; 151 G; 146 T; 0 other;
 XX SQ Alignment Scores:
 XX Pred. No.: 2,126-195
 XX Score: 203.00
 XX Percent Similarity: 100.00%
 XX Best Local Similarity: 100.00%
 XX Query Match: 99.02%
 XX Indels: 0
 XX Caps: 0
 XX DB: 22

US-09-727-770-2 (1-295) x AAK12991 (1-612)
 QY 1 MetSerAsnAsnSerProGluValAlaValPheThrIleSerGlyAlaMetAlaThr 20
 DB 3 ATGTCAACAAACAGCGCGAGTATGCTTTGTTTCAGCATCTGGGGTGTATGCCACC 62
 QY 21 MetValSerSerGlyLeuValAlaValGlyMetAlaValAsnGlyThrGlyIleMet 40
 DB 63 APGGTCTCAGTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122
 QY 41 AlaMetSerValMetTrpProGluLeuIleHisMetLysSerIleIleProValValMet 60
 DB 123 GCCATGCTGTGATGTGGCAGAGTGAATGATGATGATGATGATGATGATGATGATGATG 182
 QY 61 AlAGlyIleIleIleThrIleThrGlyLeuValAlaValProProAlaAsnSerLeuAsn 80
 DB 183 GTGTGTATCATCACCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
 QY 81 AspAspAsnSerLeuThrSerSerPheLeuGlnLeuValAlaValGlySerGlyLeuAla 100
 DB 243 GATGACAAACAGCTCTATAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
 QY 101 AlAGlyPheAlaIleValIleValGlyAspThrGlyLysGlyThrAlaGlnGlnPro 120
 DB 303 GCGAGCTTGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
 QY 121 ArgLeuPheValGlyMetIleLeuIleLeuIlePheAlaValValLeuIleLeuSerThr 140

XX Novel single exon nucleic acid probe used to measuring gene expression
 PI in a human breast
 XX Claim 25: SEQ ID No 5136; 422bp; English.
 XX the present invention relates to novel single exon nucleic acid probes,
 CC the present sequence is one such probe, the probes are useful for
 CC measuring human gene expression in a human breast sample, where the probe
 CC hybridises at high stringency to a nucleic acid expressed in the human
 CC breast. The probes are useful for predicting, diagnosing, grading,
 CC staging, monitoring and assessing prognosis of the human breast,
 CC particularly those diseases with polyclonal activity, the diseases
 CC include: breast cancer, disorders of development, inflammatory diseases
 CC of the breast, fibrocystic changes, proliferative breast disease and
 CC non-carcinoma tumors.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIP0
 CC at ftp.wipo.int/pub/ipdb/seq_01.pat_02

XX Sequence 612 BP; 120 A; 195 C; 151 G; 145 T; 0 other;

Alignment Scores:

Prod. No.: 2-126-195 Length: 612
 Score: 203.00 Matches: 203
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.02% Indels: 0
 Gaps: 0

US-09-727-770-2 (1-296) x AA105145 (1-612)

CC 1 MetSerAsnAspSerProThrAlaValPheThrLeuLeuValAlaMetAlaThr 29
 DB 3 AUGTCCAAAGAGCGCGGATGCTTTGTTTTCATGATGGGAGTCATGGGAGCC 62
 CC 21 MetValAspSerLeuValAlaValAspThrAlaValAspThrLeuValMet 10
 DB 63 ATGGTCTCAGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 122
 CC 41 AlaMetSerValMetTrpProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
 DB 123 GCGATGTCGTCATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 182
 CC 61 AlaValLeuLeuLeuLeuLeuLeuValAlaValAlaValAlaValAlaVal 80
 DB 184 GTAT 242
 CC 81 AspAspAsnSerLeuValProSerProThrLeuLeuLeuLeuLeuLeuLeu 130
 DB 243 GATACAAAGTCTGTATATATATATATATATATATATATATATATATATAT 402
 CC 101 AlaValProAlaValValValValValValValValValValValValVal 120
 DB 403 GCGGAGCTTGGTATGTCATGATGGGAGAGAGAGAGAGAGAGAGAGAGAG 362
 CC 121 AlaLeuProValValValValValValValValValValValValValVal 140
 DB 403 GAGTAT 422
 CC 141 LysGlnProLeuSerLysProThrSerHisValAlaValLysLysAspPhe 160
 DB 423 AAAT 482
 CC 161 LeuSerValGlnProAlaValHisAspValAlaValAlaValAlaValAla 180
 DB 483 TGGGAG 542
 CC 181 LeuSerValGlnProAlaValHisAspValAlaValAlaValAlaValAla 200
 DB 543 GAAAT 602
 CC 201 HisAlaVal 204

DB 603 CATGCTGTC 611
 RESULT 11
 AB312686
 ID ABS12686 standard; DNA; 612 BP.
 XX
 AC ABS12686;
 XX 19-AUG-2002 (first entry)
 XX Human genome-derived single exon probe (see Fig. 1) SEQ ID NO 12677.
 CC Human, fs, single exon probe, asthma, lung cancer, COPD, ILD,
 CC chronic obstructive pulmonary disease, interstitial lung disease;
 CC familial idiopathic pulmonary fibrosis; neurofibromatosis;
 CC tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;
 CC Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
 CC pulmonary hypertension; lymphangioma; lymphoma; Kaposi's sarcoma;
 CC pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 CC primary ciliary dyskinesia; pulmonary hypertension;
 CC hyaline membrane disease; open reading frame; ORF.
 XX Homo sapiens.
 XX W0200186004-A2.
 XX 15-NOV-2001.
 XX 30-JAN-2001: 2001WO-US000665.
 XX 04-FEB-2000: 2000US-190312P.
 XX 26-MAY-2000: 2000US-207456P.
 XX 30-JUN-2000: 2000US-060840B.
 XX 03-AUG-2000: 2000US-053236P.
 XX 21-SEP-2000: 2000US-234687P.
 XX 27-SEP-2000: 2000US-236359P.
 XX 04-OCT-2000: 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI: 2002-114184/15.
 XX Spatially addressable set of single exon nucleic acid probes, used to
 XX measure gene expression in human lung samples -

XX Claim 4, SEQ ID NO 12677; 634pp; English.

XX The invention relates to a spatially addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12487 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes, the novel set of probes which hybridise at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryotic lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray, assuring exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above; and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarray; and (c) a probe with the exon, where a specific pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exon should be assigned to a single gene; a probe comprising one

QY 61 AlaGlyIleIleThrIleTyrGlyLeuValAlaValProPheSerAlaAsnSerLeuAsn 90
 DB 256 GCTGGTAATCAACCACTATGGGATAGGGAGGCTGGGCTGGGCAACATCCGGAAT 415
 QY 81 AspAspAsnSerLeuTyrSerSerPheLeuGlnLeuGlyAlaIleValSerGlyLeuAla 100
 DB 416 GATGACACACAGCTCTATAGAGTTCTCTCCACCTGGGGCTGGGCTGGGCTGGGCTGGG 475
 QY 101 AlaGlyPheAlaIleValIleValGlyAspThrGlyTyrGlySerGlyThrAlaGlnIlePro 120
 DB 476 GCGGCTTTGGCATGCTATGCTGGAGGACACTGGCAAGTGTGGCACTGGCCAGTAGCGC 445
 QY 121 ArgLeuPheVal 124
 DB 436 CGACTATTGTA 447
 REFSeq 1.4
 ARA21582
 II ARA21582 standard; DNA: 448 BP.
 AC ARA21582:
 XX
 XX 23-JAN-2002 (first entry)
 DI
 DE Probe #48 for gene expression analysis in human heart cell sample.
 XX Human gene expression; heart, microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.
 XX
 XX Homo sapiens.
 XX W0200157274-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000666.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0642366.
 XX 21-SEP-2000; 2000US-0244687.
 XX 27-SEP-2000; 2000US-0246359.
 XX 04-OCT-2000; 2000CB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DE, Chen W, Rank DR;
 XX WPI: 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 XX hearts.
 XX
 XX claim 1: SEQ ID No 48: 530pp: English.
 XX
 XX The present invention relates to single exon nucleic acid probes for
 XX measuring human gene expression in a sample derived from human heart. The
 XX present sequence is one such probe. The probes may be used for
 XX predicting, measuring and displaying gene expression in samples derived
 XX from the human heart via microarrays. By measuring gene expression, the
 XX probes are useful for predicting, diagnosing, grading, staging,
 XX monitoring and proposing diseases of the human heart and vascular system
 XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 XX congenital heart disease.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pat_sequences
 XX
 XX Sequence 448 BP: 79 A; 147 G; 112 C; 110 T; 0 other;

Alignment Scores:
 Pred. No.: 8, 27e-116 Length: 448
 Score: 124.00 Matches: 124
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60.49% Indels: 0
 DB: 22 Gaps: 0
 US-09-727-770-2 (1-205) x ARA21582 (1-448)
 QY 1 MetSerAsnAsnSerProGluTyrAlaLeuValPheThrIleSerGlyAlaMetAlaThr 20
 DB 76 ATGTGTAACAAACAGGAGGAGTATGCTTTGGTTTTCACATATCGGGTGTATGGCCACC 135
 QY 21 MetValSerSerGlyLeuGlyAlaValAspGlyMetAlaValAspGlyThrGlyIleMet 40
 DB 136 ATGCTCTGGAGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 195
 QY 41 AlaMetSerValMetTyrProGluLeuIleHisMetLysSerIleIleProValValMet 60
 DB 196 GCCAAGCTCTGCACTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 255
 QY 61 AlaGlyIleIleThrIleTyrGlyLeuValAlaValProProAlaAsnSerLeuAsn 80
 DB 256 GCTGTATATCATCACATATGAGCTAGGGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 415
 QY 81 AspAspAsnSerLeuTyrSerSerPheLeuGlnLeuGlyAlaIleValSerGlyLeuAla 100
 DB 416 GATGACACACAGCTCTATAGAGTTCTCTCCACCTGGGGCTGGGCTGGGCTGGGCTGGG 475
 QY 101 AlaGlyPheAlaIleValIleValGlyAspThrGlyTyrGlySerGlyThrAlaGlnIlePro 120
 DB 476 GCGGCTTTGGCATGCTATGCTGGAGGACACTGGCAAGTGTGGCACTGGCCAGTAGCGC 445
 QY 121 ArgLeuPheVal 124
 DB 436 CGACTATTGTA 447
 RESULT 14
 AAK00062
 ID AAK00062 standard; DNA: 448 BP
 XX
 XX AAK00062:
 XX
 XX 05-NOV-2001 (first entry)
 XX Human brain expressed single exon probe SEQ ID NO: 53.
 XX
 XX Human brain expressed exon gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer; ss.
 XX
 XX Homo sapiens.
 XX
 XX W0200157275-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000667.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0642366.
 XX 21-SEP-2000; 2000US-0244687.
 XX 27-SEP-2000; 2000US-0246359.
 XX 04-OCT-2000; 2000CB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DE, Chen W, Rank DR;
 XX WPI: 2001-488446/52.
 XX

CC activity. The polynucleotide may also be useful for gene therapy.

XX Sequence 136 BP; 24 A, 35 C, 26 G, 24 T; 0 other;

Alignment Scores:
 Pred. No.: 0.000221 Length: 109
 Score: 14.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.34% Indels: 0
 DB: 20 Gaps: 0

US-09-727-770-2 (1-205) x AAS8403 (1-109)

QY 52 MetlySerrilleProValMetAlaClyThelle 64

DB 5 ATGAAGTCATCAATCCAGTGGTCATGGTCGATGATC 43

RESULT 36

ID AAS8403

QY AAS8403 standard; cDNA: 541 BP.

XX AAS8403;

XX 14-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #19207.

XX Human: chromosome mapping; gene mapping; gene therapy; forensics;
 XX food supplement; medical imaging; diagnostics; genetic disorder; ss.

XX Homo sapiens

XX W0200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-0208641.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0640167.

XX (HYPH-) HVSEQ INC.

XX Drmanac RT, Liu C, Tanu YT.

XX W01-2301-639462/73.

XX P-PSDB: ABL19215.

XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits and to assess
 XX biodiversity.

XX Claim 1: SEQ ID No 19207; 104pp; English.

XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 XX and gene mapping, and in recombinant production of (II). The
 XX polynucleotides are also used in diagnostics as expressed sequence tags
 XX for identifying expressed genes. (I) is useful in gene therapy techniques
 XX to restore normal activity of (II) or to treat disease states involving
 XX (II). (II) is useful for generating antibodies against it, detecting or
 XX quantitating a polypeptide in tissue, as molecular weight markers and as
 XX a food supplement. (II) and its binding partners are useful in medical
 XX imaging of sites expressing (II). (I) and (II) are useful for treating
 XX disorders involving aberrant protein expression or biological activity.
 XX The polypeptide and polynucleotide sequences have applications in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits and to assess biodiversity
 XX and to produce other types of data and products dependent on DNA and
 XX amino acid sequences. AAS64197-AAS94564 represent novel human

CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 541 BP, 83 A, 166 C, 134 G, 138 T, 20 other;

Alignment Scores:
 Pred. No.: 0.00102 Length: 541
 Score: 14.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.34% Indels: 0
 DB: 23 Gaps: 0

US-09-727-770-2 (1-205) x AAS83403 (1-541)

QY 52 MetlySerrilleProValMetAlaClyThelle 64

DB 199 ATGAAGTCATCAATCCAGTGGTCATGGTCGATGATC 237

RESULT 37

ABL11647

ID ABL11647 standard; cDNA: 582 BP.

XX ABL11647;

XX ABL11647;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 29424.
 XX Drosophila: developmental biology; cell signalling; insecticide;
 XX pharmaceutical; gene; ss.

XX Drosophila melanogaster.

XX W0200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-0509231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWB, Myers EW;

XX W01-256969/75.

XX P-PSDB: ABL67544.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 XX interactions.

XX Claim 1: SEQ ID NO 29424, 21pp; Sequence listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 XX capable of detecting 1000 or more genes from Drosophila. The invention is
 XX useful in developmental biology and in elucidating cell signalling and
 XX cell-cell interactions in higher eukaryotes for the development of
 XX insecticides, therapeutics and pharmaceutical drugs. The invention
 XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 XX sequences (ABL01840-ABL16175) and the encoded proteins
 XX (ABD5737-ABD72072).

XX The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 582 BP, 155 A, 153 C, 170 G, 150 T, 0 other;

Alignment Scores:

us-09-727-770-2.olil0p2n.rng

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PR 24-JUN-1999; 990S-0140695;
PR 28-JUN-1999; 990S-0140824;
PR 29-JUN-1999; 990S-0140891;
PR 30-JUN-1999; 990S-0141287;
PR 01-JUL-1999; 990S-0141842;
PR 01-JUL-1999; 990S-0142154;
PR 02-JUL-1999; 990S-0142055;
PR 06-JUL-1999; 990S-0142390;
PR 08-JUL-1999; 990S-0142801;
PR 09-JUL-1999; 990S-0142920;
PR 12-JUL-1999; 990S-0142977;
PR 13-JUL-1999; 990S-0143542;
PR 14-JUL-1999; 990S-0143624;
PR 15-JUL-1999; 990S-0144005;
PR 16-JUL-1999; 990S-0144085;
PR 16-JUL-1999; 990S-0144086;
PR 19-JUL-1999; 990S-0144325;
PR 19-JUL-1999; 990S-0144331;
PR 19-JUL-1999; 990S-0144332;
PR 19-JUL-1999; 990S-0144333;
PR 19-JUL-1999; 990S-0144334;
PR 19-JUL-1999; 990S-0144335;
PR 20-JUL-1999; 990S-0144352;
PR 20-JUL-1999; 990S-0144632;
PR 20-JUL-1999; 990S-0144684;
PR 21-JUL-1999; 990S-0144814;
PR 21-JUL-1999; 990S-0145086;
PR 21-JUL-1999; 990S-0145088;
PR 22-JUL-1999; 990S-0145085;
PR 22-JUL-1999; 990S-0145089;
PR 22-JUL-1999; 990S-0145192;
PR 23-JUL-1999; 990S-0145145;
PR 23-JUL-1999; 990S-0145218;
PR 23-JUL-1999; 990S-0145224;
PR 26-JUL-1999; 990S-0145276;
PR 27-JUL-1999; 990S-0145913;
PR 27-JUL-1999; 990S-0145918;
PR 27-JUL-1999; 990S-0145919;
PR 28-JUL-1999; 990S-0145951;
PR 02-AUG-1999; 990S-0146386;
PR 02-AUG-1999; 990S-0146388;
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

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Tue Dec 31 14:03:13 2002

us-09-727-770-2.oli10p2n.rng

PF Novel nucleic acid sequences isolated from germinating seeds encoding
 PT polypeptides that are useful to control seed germination in plants -
 PS Claim 19; Page 55; 63pp; English.
 XX The present invention relates to enzymes such as seed-specific
 CC endo-beta-mannase (e.g., lycopersicon esculentum (le) MAN2),
 CC polygalacturonase (PG) (e.g., leXPGL), cellulases such as Cel55 and
 CC Cel68, arabinosidase (e.g., leAAR), α -glucanase, α -xylosidase,
 CC (XET) (e.g., leXET4) and expansins such as leEXP4, leEXP8 and leEXP10
 CC isolated from germinating seeds. All these enzymes are expressed
 CC initially in the endosperm caps and are associated with cell wall
 CC hydrolysis. These enzymes are associated with weakening of tissues
 CC surrounding the embryo and/or initiating radicle growth, the control of
 CC expression of these endogenous genes is therefore a convenient means for
 CC controlling seed germination. The present sequence is
 CC lycopersicon esculentum (tomato) vacuolar proton-translocating ATPase
 CC (LVA-p1) cDNA, which is related to the invention.

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US 09-727-770-2 (1 295) x AA004714 (1 900)

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KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

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US-09-727-770-2 (1-205) x AAC47752 (1-977)
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KW pathway; promoter; termination sequence; corn; ss.
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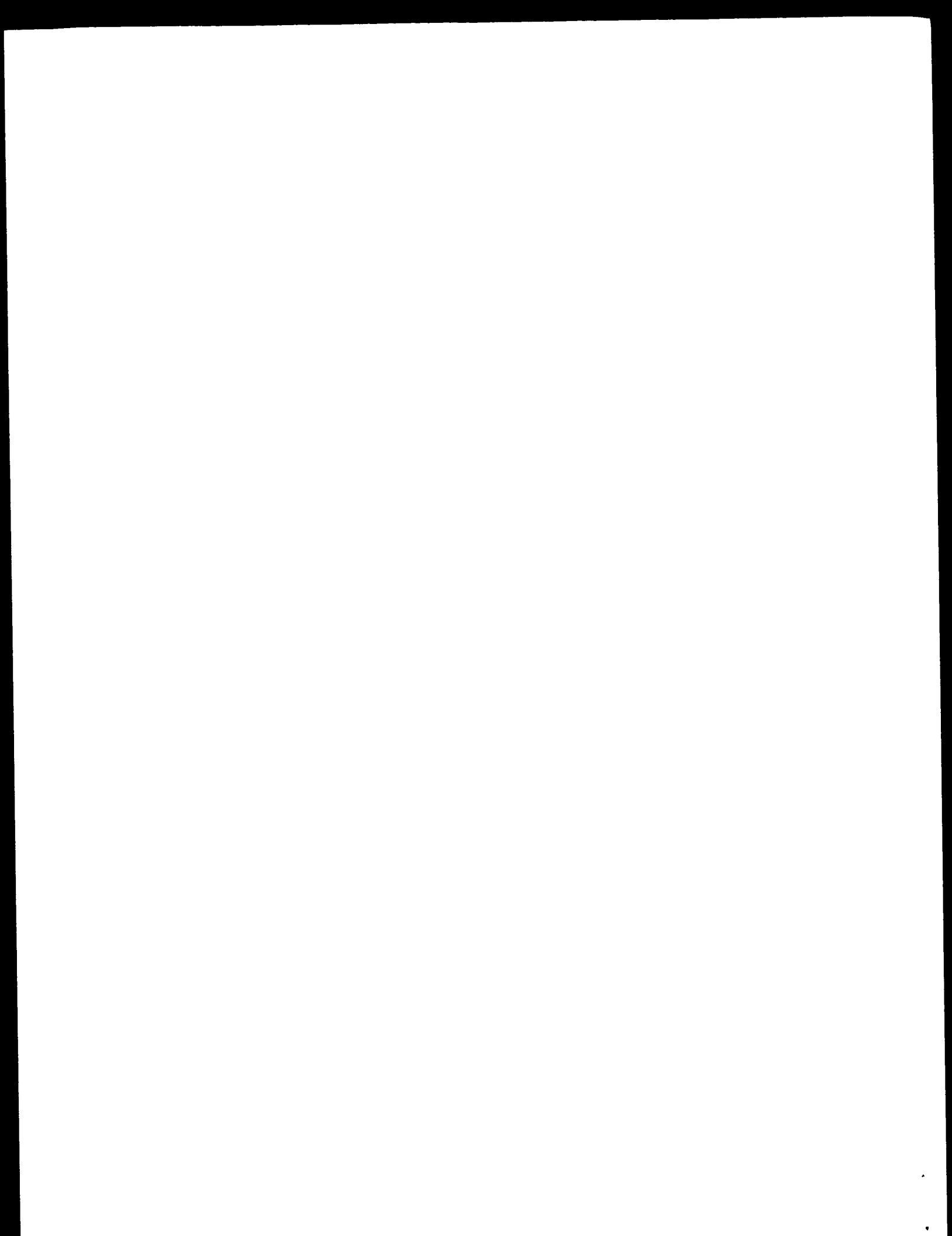
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JOURNAL MEDLINE CONTACTS: Simpson A.J.G., Laboratory of Cancer Genetics, Ludwig Institute for Cancer Research, Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704022 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICP Human Cancer Genome Project. This entry can be seen in the following URL:
<http://www.ludwig-lab.org/human/cancer/genome/fapsp/lcp/>
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Tel: +55-11-2704022 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br
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Tel: +55-11-2704022 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br
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<http://www.ludwig-lab.org/human/cancer/genome/fapsp/lcp/>
Seq primer: puc18 forward High quality sequence start: 56 High quality sequence stop: 149.
Location/Qualifiers location: 1..149 /organism="Homo sapiens" /db_xref="taxon:9606" /feature_111="c16164" /dev_stage="Adult" /note="Organ: colon;ins: Vector: puc18; Site: Small; Site 2: Small; A mini-library was made by cloning products derived from GAPDS cDNA (U.S. Patents Patent application No. 196,716 Ludwig Institute for Cancer Research) profiles into the puc18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." base_count 32 4 20 2 59 4 27 1 origin BASIS ORIGIN Alignment Scores: Prod. No.: 3,950-09 Length: 149 Score: 19.00 Matches: 19 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 9.27% Indels: 0 DB: 12 Gaps: 0 US-09 727 770 2 (1-205) x BF819273 (1 149)
CY 115 CTTGTAATCTGGTCAAGTACCTGTGCGAATGCTTCCTCCTGCTCTCCATCTCCATA 133
DE 145 GGACGCCGACGACAGCCGCAGTACTACGAGCATGAAGCCGATTCATCATCTGCGC 89
RESULT 4
BF819278/C LOCUS BF819278 189 bp mRNA linear EST 13-JAN-2000 DEFINITION Homo sapiens BMD-9 Homo sapiens cDNA, mRNA sequence. ACCESSION BF819278 VERSION 1 KEYWORDS EST. SOURCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 189) AUTHORS Nuzzi, M.A., da Silva W Jr., Zetter, M.A., Bordin, S.O., Costa, F.F., Priores, M.R., Goldman, C.H., Carvalho, A.P., Matsubara, A., Latta, V.S., Simpson, A.J.G., Brunstein, A., de Oliveira, P.S., Pachter, P., Jongsomchai, V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.G. SHOTGUN SEQUENCING OF THE HUMAN TRANSCRIPTOME WITH ORF EXPRESSED SEQUENCE TAGS. JOURNAL MEDLINE CONTACTS: Simpson A.J.G., Laboratory of Cancer Genetics, Ludwig Institute for Cancer Research, Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704022 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICP Human Cancer Genome Project. This entry can be seen in the following URL:
<http://www.ludwig-lab.org/human/cancer/genome/fapsp/lcp/>
Seq primer: puc18 forward High quality sequence start: 56 High quality sequence stop: 149.
Location/Qualifiers location: 1..149 /organism="Homo sapiens" /db_xref="taxon:9606" /feature_111="c16164" /dev_stage="Adult" /note="Organ: colon;ins: Vector: puc18; Site: Small; Site 2: Small; A mini-library was made by cloning products derived from GAPDS cDNA (U.S. Patents Patent application No. 196,716 Ludwig Institute for Cancer Research) profiles into the puc18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." base_count 32 4 20 2 59 4 27 1 origin BASIS ORIGIN Alignment Scores: Prod. No.: 3,950-09 Length: 149 Score: 19.00 Matches: 19 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 9.27% Indels: 0 DB: 12 Gaps: 0 US-09 727 770 2 (1-205) x BF819273 (1 149)
CY 115 CTT

Brazil
Tel.: +56-11-2704922 Fax: +56-11-2707001 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL: http://www.ludwig.lu.se/human/cancer/genome/index.html#seq
Seq primer: puc 18 forward High quality sequence start: 24 High quality sequence stop: 189. Location/Qualifiers catalase : c_189 organism "Homo sapiens" db_xref="taxon:9606" clone_lib="cl0194" dev_stage:"Adult"
Note: Organ: colon; Ins: Vector: puc18; Site: SmaI; Site-2: SmaI: A mini-library was made by cloning products derived from CRISTES PCP (U.S. letters Patent application No. 199,716 - Ludwig Institute for Cancer Research) profiled into the PCR vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
BASE COUNT 39 a 40 C 39 t
ORIGIN
Alignment Scores:
Pred. No.: 5,32e-09 Length: 189
Score: 19,00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best local similarity: 100.00%
Query Match: 9.27%
DB: 12 Mismatches: 0
0 Indels: 0
0 Gaps: 0
US-09-727-770-2 (1-295) x BP819278 (1-189)
QY 115 GlyThrAlaGlnGInProArgLeuApheValClyMetileleuLieuLeullepheAala 133 Db 185 GCCACCCCGAGCACGCCGCACATATTGGTGAAGAACAATCTCATTCCTTGSCC 129
RESULT 4
AL585139/C
Locus
DEFINITION AL585139 BP Chicken Embryo Library Gallus gallus cDNA clone
ACCSSION AL585139
VERSION AL585139.1 GI:13163872
KEYWORDS EST.
SOURCE
ORGANISM
Gallus gallus
Eukaryote; Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi;
Aves, Neognathae, Galliformes, Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 203)
Murray,P.
Fp chicken Embryo Library
Unpublished (2001)
Contact: Fraser Murray
Dept. Genomics and Bioinformatics
Koslin Institute
Peshin, Midwayville, KY25 qps, UK
Tel: +44 (0)131 627 4200
Fax: +44 (0)131 440 0434
Email: fraser.murray@btis.ac.uk
Seq primer: 13,
Location/Qualifiers catalase : c_203 organism-"Gallus gallus" db_xref="taxon:9031" clone="ROS019C04" clone_lib="FP Chicken Embryo Library" Issue type: "Embryo"
FEATURES
SOURCE

[illegible]


```

Query Match: 9.27% Indels: 0
DB: 14 Gaps: 0

US-09-727-770-2 (1-295) x BM619587 (1-464)

QY 115 GlyThrAlaGlnGlnProArqLeupheValGlyMetIleLeuIleLeuIlePheAla 133
|||||
DB 178 GGTACTGGCGACAGCGGAGCTGTCTGGTGGTATGATCGTCAATTCATTCGGG 234

RESULT 36
LOCUS BE654182 465 bp mRNA linear EST 06-SEP-2000
DEFINITION U1-M-ANI-ale-c-06-0-01-11 NIH-BMAP-MBC-N Mus musculus cDNA clone
|||||
U1-M-ANI-ale-c-06-0-01 5', mRNA sequence.
ACCESSION BE654182
VERSION BE654182.1 GI:9480095
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 465)
AUTHORS Ronaldo, M.F., Lennon, G., and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery. Genome Res 6 (9), 791-806 (1996)
JOURNAL Genome Res
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd., Room 7H 7190, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mbe@mail.nih.gov
cDNA Library Preparation: M.B. Soares Lab. Cloning distribution.
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements.
Seq primer: M13 Reverse.
FEATURES
Source
Location/Qualifiers
1..465
/organism="Mus musculus"
/sra_id="5781761"
/db_xref="taxon:10090"
/clone_lib="U1 M ANI ale c 06-0-01"
/clone_host="NIH-BMAP-MBC-N"
/seq_start="27-72 bp"
/seq_end="27-72 bp"
/seq_host="pH10B"
/seq_vector="pT7D-pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; The
NIH-BMAP-MBC-N library is a normalized library constructed
from mouse basal ganglia. The tag is a string of 5
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Ronaldo, Lennon and Soares, Genome Research 6: 791-806
(1996). Tissue provided by Dr. Andre Nedevich,
Zivic-Miller Laboratories."
BASE COUNT 81 a 147 c 118 g 119 t
ORIGIN
Alignment Scores:
Prod. No.: 1,630-08 Length: 465
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservations: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.27% Indels: 0
Gaps: 10
US-09-727-770-2 (1-295) x BE654182 (1-465)

QY 115 GlyThrAlaGlnGlnProArqLeupheValGlyMetIleLeuIleLeuIlePheAla 133
|||||
DB 114 GGCACGGCGACAGCGGAGCTATTTCGCGATGATCGTCAATTCATTCGGG 169

RESULT 48
LOCUS BE601869 474 bp mRNA linear EST 25 APR 2001
DEFINITION BE601869 MARC 380V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE601869
VERSION BE601869.1 GI:11695092
KEYWORDS EST.
SOURCE Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


Tel: 402 762 4366
 Fax: 402 762 4360
 Email: smithemall.mar.usda.gov
 Single pass sequencing. Bases called and all trimmed with phred v0.980/04.e. Vector identified by cross_match with the minscore 18 and -mismatch 12 options.

PCR primers
 FORWARD: AGCAACACGATACACAT
 BACKWARD: GTTTCACGATGACGACG
 Plate: 79 row: K column: 12
 Seq primer: ATTAGGTCGACATAG.
 Location/Qualifiers
 1..489
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MAGE 3BOV"
 /issue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV sport6, site_1: NotI; Site_2: SalI;
 Library made from pooled tissue from marrow, alveolar
 macrophage, ovary, fetal semitendinosus muscle, and fetal
 Longissimus muscle."
 74 a 189 c 134 q 92 t

BASE COUNT
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,740-08 Length: 489
 Score: 19.00 Matches: 19
 Percent Similarity: 100.00% Mismatches: 0
 Best local similarity: 100.00% Conserved: 0
 Query Match: 9,27% Indels: 0
 Gaps: 0
 DH: 12

US-09-727 770-2 (1-205) x RP796928 (1-489)
 QY 115 GlyThrAlaGlnGlnProArgLeuPheValGlyMetIleleuIleleuIleleuAla 133
 DB 112 GGCACGCGCGACGACGCGCGCTCTCTGGTCATGATGATCTGATCTGCGC 168

RESULT 41
 BE276276
 LOCUS
 DEFINITION
 BE276276 mRNA 491 bp mRNA linear EST 13-JUL-2000
 531144381F1 R18_MCC_20 Homo sapiens cDNA clone IMAGE:4050036 5'.

ACCESSION
 BE276276
 VERSION
 BE276276.1 GI:9512394
 KEYWORDS
 EST.

SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

1. (bases 1 to 491)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Contact: Robert Strausberg, Ph.D.
 Email: rstraus@nhi.nih.gov
 Tissue Procurement: ATCC/Genetic
 cDNA Library Preparation: Lindberg/Rubin Laboratory
 cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLC95 row: b column: 21
 High quality sequence stop: 489.
 Location/Qualifiers
 1..491
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4050036"
 /issue_type="DH10B" 20
 /lab_host="DH10B (phage-resistant)"

FEATURES
 SOURCE
 Location/Qualifiers
 1..491
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4050036"
 /issue_type="DH10B" 20
 /lab_host="DH10B (phage-resistant)"

/note "Organism: skin; Vector: pCR7; Site_1: XbaI; Site_2:
 EcoRI; cDNA made by oligo dt primed. Birectionally
 cloned into EcoRI/XbaI sites using the following 5'
 adaptor: GGTACAGAG(G). Size selected 500bp for average
 insert size 1.8kb. Library constructed by Lindberg
 the laboratory of Gertal M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and SuperScript II RT (Life Technologies)."
 74 a 176 c 147 q 95 t

Alignment Scores:
 Pred. No.: 1,750-08 Length: 491
 Score: 19.00 Matches: 19
 Percent Similarity: 100.00% Mismatches: 0
 Best local similarity: 100.00% Conserved: 0
 Query Match: 9,27% Indels: 0
 Gaps: 0
 DH: 10

US-09-727 770-2 (1-205) x BE276276 (1-491)
 QY 115 GlyThrAlaGlnGlnProArgLeuPheValGlyMetIleleuIleleuIleleuAla 143
 DB 412 GGCACGCGCGACGACGCGCGCTCTCTGGTCATGATGATCTGCGC 468

RESULT 42
 AW768111
 LOCUS
 DEFINITION
 AW768111 496 bp mRNA linear EST 16 FEB 2001
 d371b92.y1 Harland stage 19 23 Xenopus laevis cDNA clone
 IMAGE:4200551 5' similar to qd.Mc2/ba.VA566AA AT 5'UT; IMAGE:16 20
 PROTEOLIPID SUBUNIT (HUMAN). qd.Mc4239 Mouse vacuolar H(+) ATPase
 (MOUSE); mRNA sequence.

ACCESSION
 AW768111
 VERSION
 AW768111.1 GI:7700194
 KEYWORDS
 EST.

SOURCE
 ORGANISM
 African clawed frog.
 Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 Xenopodidae; Xenopus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

1. (bases 1 to 496)
 Clifton, S., Johnson, S., L., Blumberg, R., Som, J., Hillier, L., Papo, D.,
 Martin, J., Wylic, J., Underwood, K., Theis, B., Bowers, Y., Person,
 B., Gibbons, M., Harvey, N., Ketter, J., Jackson, J., McCann, P.,
 Waterston, R., and Wilson, R.
 WashU Xenopus EST project, 1999
 Unpublished (1999)
 Contact: Sandy Clifton, Ph.D.
 WashU Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8601, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est.watson.wustl.edu
 Library constructed by R. Harland, PhD (University of California,
 Berkeley)

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LLNL at:
 image.llnl.gov/image/htmi/consortium.shtml
 Seq primer: 40bp from cDNA
 High quality sequence stop: 492.
 Location/Qualifiers
 1..496
 /organism="Xenopus laevis"
 /db_xref="taxon:8345"
 /clone_image="4200551"
 /issue_type="Harland stage 19 23"
 /lab_host="stage 19 23"
 /issue_type="neurala"
 /lab_host="stage 19 23"
 /note "Vector: pCR7 (custom); Site_1: NotI; Site_2: SalI
 ; cDNA made by oligo dt primed. Library constructed by

FEATURES
 SOURCE
 Location/Qualifiers
 1..496
 /organism="Xenopus laevis"
 /db_xref="taxon:8345"
 /clone_image="4200551"
 /issue_type="Harland stage 19 23"
 /lab_host="stage 19 23"
 /issue_type="neurala"
 /lab_host="stage 19 23"
 /note "Vector: pCR7 (custom); Site_1: NotI; Site_2: SalI
 ; cDNA made by oligo dt primed. Library constructed by


```

RESULT 47
RG235129
LOCUS
DEFINITION
ACCESSION
RG235129
VERSION
RG235129.1
KEYWORDS
EST.
SOURCE
dog.
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 504)
AUTHORS
O'Shaughnessy A., Palmer J., McGuffee W.R., Baker J.P., Baheti A.,
Cannius D., Dedhar N., de la Bastide M., Katzenberger F., King
J., Kirchoff K.A., Miller R., Muller S., Raschendorf U., Preston
J.R., Shah P.S., Spiegel J.A., Zuberhorn G., Zuberhorn J., and Hannon
G.J.
TITLE
Expressed sequence tags from Canis familiaris (dog) (5_2002)
JOURNAL
Unpublished (2002)
COMMENT
Contact: W. Richard McGuffee
Lita Anderson, Helen Kunko, Stephen J. Zuberhorn
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcguffee@cshl.org
Plate: hd54 row: c column: 09
Seq primer: -21M33a1vrev
High quality sequence stop: 504.
FEATURES
source
location/qualifiers
1..504
/organism="Canis familiaris"
/db_xref="taxon:9615"
/clone="hd54009"
/notes="Vector: lambda Zap II; The library was provided by
Grega Hannon and Joe Saxon (Cold Spring Harbor Laboratory
). This library is oligo(dT) primed using Stratagene zap
cDNA synthesis kit. It was made from dog whole brain
cells. Please contact Grega Hannon (hannon@cshl.org) with
any library related inquiries."
BASE COUNT
88 a 171 c 144 g 111 t
ORIGIN
Alignment Scores:
Pred. No.: 1,80e-08 Length: 504
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 9.27% Indels: 0
DB: 14 Gaps: 0
US-09 727-770-2 (1-205) x RG235129 (1-504)
Q7 115 GlythralaGlnProArgLeuValGlyMetLeuLeuLeuPheAla 133
|||||
DB 104 GGCATCGCCGACGACGCTGCTATTCGTCGACATGCTGATGCTGATTCGCTGCG 160
RESULT 48
RG10745
LOCUS
DEFINITION
ACCESSION
RG10745
VERSION
RG10745.1
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 507)

```

```

AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rcp@nci.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
cDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1551 row: m column: 05
High quality sequence stop: 428.
FEATURES
source
location/qualifiers
1..507
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5219500"
/clone_lib="RHLMGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/notes="Vector: pCMV-script; Plasmid: Rel1, Site 2; EcoRV
(digested); RNA source: leukocytes from anonymous pool of
newly activated adult donors. Library is oligo(dT) primed
and directionally cloned (kcoRV site is destroyed upon
cloning). Average insert size: 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH-MGC Library."
BASE COUNT
106 a 169 c 155 g 97 t
ORIGIN
Alignment Scores:
Pred. No.: 1,82e-08 Length: 507
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 9.27% Indels: 0
DB: 13 Gaps: 0
US-09 727-770-2 (1-205) x BG19735 (1-507)
Q7 115 GlythralaGlnProArgLeuValGlyMetLeuLeuLeuPheAla 133
|||||
DB 163 GGCATCGCCGACGACGCTGCTATTCGTCGACATGCTGATGCTGATTCGCTGCG 219
RESULT 49
RG345676
LOCUS
DEFINITION
ACCESSION
RG345676
VERSION
RG345676.1
KEYWORDS
EST.
SOURCE
African clawed frog.
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE
1 (bases 1 to 512)
AUTHORS
Clifton S., Johnson S.L., Blomstedt K., Scott J., Hillier L., Pape D.,
Ab., Gibbons M., Harvey R., Underwood K., Theisind K., Howets V., Person
J., Martin J., Wylic, J., Greenwood K., Kitter J., Jackson J., McCann K.,
Waterston R., and Wilson R.
WashU Xenopus EST project, 1999
Unpublished (1999)
CONTACT: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

```

Tel: 414 286 1800
Fax: 414 286 1810

Email: estw@wustl.edu

Library constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B. Gurdon, (Wellcome/CRC Institute). DNA Sequencing by: Washington

University Genome Sequencing Center

clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

Seq primer: -40RP from Gibco

High quality sequence stop: 459.

Location/Qualifiers

FEATURES

source

1..512
/organism="Xenopus laevis"
/db_xref="taxon:8356"
/clone="IMAGE:3431578"
/clone_lib="Wellcome CRC p30NA1 eqq"
/lab_host="DH10B (phage resistant)"
/issue_type="eqq"
/note="Vector: pGEM1, Site 1, NotI, Site 2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Library was constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)."
116 a 127 c 108 q 161 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 1,84e-08 Length: 512
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.27% Indels: 0
DB: 12 Gaps: 0

US-09 727-770-2 (1-205) x BG445676 (1-512)

QY 115 GYThrAlaGlnProArgLeuValGlyMetIleLeuIleLeuIlePheAla 133

DB 209 GGIACAGCACACCAACCTGGACTATTCTGGGAATGATCTCATCTTCGCA 265

RESULT 50

AL644755

LOCUS

DEFINITION AL644755 X3C-egg Silurana tropicalis cDNA clone 1164q09 5', mRNA

sequence.

ACCESSION AL644755

VERSION AL644755.1 GI:16796880

KEYWORDS EST.

SOURCE western clawed frog.

ORGANISM Silurana tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Silurana.

Huckle, E., Taylor, P., Ashurst, J., Zorn, A.M., and Rogers, J.

1 (bases 1 to 513)

Sanjour Xenopus tropicalis EST project 2001 (10_2001)

Unpublished (2001)

Contact: Huckle E

Sanjour Centre

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanjour.ac.uk

Sanjour Xenopus tropicalis EST project 2001

TROPICALIS_SEQUENCE_ID: 1164q09.sp6

Sequencing primer: SP6

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

Location/Qualifiers

1..513

/organism="Silurana tropicalis"

/db_xref="taxon:8364"

/clone="1164q09"

/clone_lib="XGC-egg"

/dev_stage="eqq"

/lab_host="Escherichia coli XL1-blue"

FEATURES

source

/note "Vector: pGS107; Site 1: EcoRI, Site 2: NotI; cDNA was oligo dT primed from 5' end of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pGS107 with EcoRI at the 5' end and NotI at the 3' end"

BASE COUNT 92 a 144 c 149 q 148 t

ORIGIN

Alignment Scores:

Pred. No.: 1,84e-08 Length: 513
Score: 19.00 Matches: 19
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.27% Indels: 0
DB: 9 Gaps: 0

US-09 727-770-2 (1-205) x AL644755 (1-513)

QY 115 GYThrAlaGlnProArgLeuValGlyMetIleLeuIleLeuIlePheAla 133

DB 432 GGIACAGCACACCAACCTGGACTATTCTGGGAATGATCTCATCTTCGCA 488

Search completed: December 28, 2002, 14:43:40

Job time : 2006 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n mode

Run on: December 28, 2002, 12:21:16 ; Search time 49 Seconds
(without alignments)
1284.045 Million cell updates/sec

Title: US-09-727-770-2
Perfect score: 205
Sequence: 1 MSNSPYALVFISGAMAT.....PEVHPLAAPPPIPIHADI 205

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 44162 seqs, 15338381 residues

Word size: 10

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MOML frame_p2n model -DEV xllh
-DB-Issued_Patents_NA -OML-Fastap -SUFFIX OLIL0P2N.rni -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX OLIGO
-TRANS=human4.0 -di -LIST=1000 -LOCAL=200 -THR SCORE=quality -THR_MIN=10
-ALIGN=50 -MSE=LOCAL -OPTIM=ELC -MSE=ext -HEATSIZE 500 -MINLEN=0
-MAXLEN=200000000 -USER=050727770 -GEN=1.1.17 -format=27122002_084548_6378
-NCPUS=6 -ICPU=4 -NO_XLPHY -NO_MMAL -LARGEQUERY -REF_SCORES 0 -WAIT 1 -LANGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FCAPOP=6
-FCAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:
1: 050727770_1.1.17_084548_6378_5A_CMB.seq**
2: 050727770_1.1.17_084548_6378_6B_CMB.seq**
3: 050727770_1.1.17_084548_6378_6A_CMB.seq**
4: 050727770_1.1.17_084548_6378_6C_CMB.seq**
5: 050727770_1.1.17_084548_6378_6D_CMB.seq**
6: 050727770_1.1.17_084548_6378_6E_CMB.seq**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
------------	-------	-------------	-----------	----	-------------

No matches found

Search completed: December 28, 2002, 13:43:55
Job time : 49 secs

The first part of the paper discusses the importance of the study and the objectives of the research. It highlights the need for a comprehensive understanding of the subject matter and the role of the researcher in this process. The second part of the paper presents the methodology used in the study, including the data collection methods and the analysis techniques. The third part of the paper discusses the results of the study and the conclusions drawn from the findings. The final part of the paper provides a summary of the key points and offers suggestions for future research.

The study was conducted in a systematic and rigorous manner, following the principles of scientific research. The data was collected from a large sample of participants, and the results were analyzed using advanced statistical techniques. The findings of the study are presented in a clear and concise manner, allowing for a thorough understanding of the subject matter. The conclusions drawn from the findings are based on a careful analysis of the data and are supported by the results of the study.

The study has several limitations, which are discussed in the paper. These limitations include the sample size, the duration of the study, and the potential for bias. Despite these limitations, the study provides valuable insights into the subject matter and contributes to the existing body of knowledge. The findings of the study are discussed in the context of the current research and are compared with the results of other studies.

The study has several strengths, which are also discussed in the paper. These strengths include the use of a large sample size, the application of advanced statistical techniques, and the thoroughness of the analysis. The study also has several practical implications, which are discussed in the paper. These implications include the need for further research in this area and the potential for the findings to be applied in practice.

In conclusion, the study provides a comprehensive understanding of the subject matter and contributes to the existing body of knowledge. The findings of the study are presented in a clear and concise manner, allowing for a thorough understanding of the subject matter. The conclusions drawn from the findings are based on a careful analysis of the data and are supported by the results of the study.


```

2 PRIOR APPLICATION NUMBER: US 09/098,409
2 PRIOR FILING DATE: 2000-06-30
2 PRIOR APPLICATION NUMBER: US 09/774,203
2 PRIOR FILING DATE: 2001-01-29
2 NUMBER OF SEQ ID NOS: 49117
2 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
2 SEQ ID NO 15890
2 LENGTH: 612
2 TYPE: DNA
2 ORGANISM: Homo sapiens
2 FEATURE:
2 OTHER INFORMATION: MAP TO AC095972.2
2 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.7
2 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.9
2 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.9
2 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.7
2 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.6
2 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5
2 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
2 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 15
2 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1
2 OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 6.4
2 OTHER INFORMATION: NT HIT: 34562332, EVALUO 9.00E-39
2 OTHER INFORMATION: EST HUMAN HIT: BF526960.1, EVALUO 1.00E-38
2 OTHER INFORMATION: SWISSPROT hit: P25956, EVALUO 1.00E-29
us-09-864-761-16890

Alignment Scores:
Prod. No.: 9-56e-196 Length: 612
Score: 204.00 Matches: 204
Percent Similarity: 100.00 Conservation: 0
Best Local Similarity: 100.00 Mismatches: 0
Query Max: 94.129 Indels: 0
DB: 10 Gaps: 0

US 09-727 770 2 (1 205) x US-09-864-761-16890 (1-612)

QY 1 MetSerAsnSerProGluTyrAlaLeuValPheThrIleSerGlyAlaMetAlaThr 20
DB 3 ATGTCAACAAACACGCGCCGACGATGCTTGGCTTTTACCAATCGGAGTCTATGCGACG 62
QY 21 MetValSerSerGlyLeuGlyAlaAlaCysGlyMetAlaLysAsnGlyThrGlyIleMet 40
DB 63 ATGGTCTTCAGTGGCGCTGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGT 122
QY 41 AlaMetSerValMetTyrPheGluGluPheHisMetLysSerAlaIleValValMet 60
DB 123 GGCATCTGTGTCATGTGGCAGACGCTATCCATCAATCAAGTGTATATGTGTATGTGTATG 182
QY 61 AlaGlyIleIleThrIleTyrGlyLeuValAlaAlaValProProAlaAsnSerLeuAsn 80
DB 183 GCTGGTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 242
QY 61 AspAspSerLeuTyrSerSerPheLeuGluLeuGlyAlaGlyLeuSerGlyLeuAla 100
DB 243 AATGACAAAGAGTGTATAGCAGTTCCTGCTAGCTGAGGAGGCTGAGGAGGAGGAGGAG 302
QY 101 AlaGlyPheAlaIleValIleValIleValAspSerGlyGlySerGlyThrAlaGlyGluPro 120
DB 403 GAGGGGTTTGCCATGTCATGCTGCGGAGACATGGTANGTGTGACATGGTGGACAGACG 362
QY 121 ArgLeuPheValGlyMetIleLeuIleLeuIlePheAlaLysValIleuIleLeuSerThr 140
DB 463 CGACTATTCTAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 422
QY 141 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 482
DB 423 AAGTAGGGGCTCTCAAAAGCCCAATATCAAAATAGATGATGATGATGATGATGATGATG 482
QY 161 PheArgAspLysGlnProAspThrHisValLeuGlySerThrProSerValValAspLeu 180
DB 404 TTGGGAAATAACAGAGTACAGAAATGATGATGATGATGATGATGATGATGATGATGATG 542

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QY 181 LeuSerValCysGlySerIleGluValHisAspLeuLeuAlaAlaGlyPheLeuPhePro 200
DB 543 CTAAGTGTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 602
QY 201 HisAlaVal 203
DB 603 CATGCTGTGC 611

RESULT 4
us-09-864-761-48
: Sequence 48, Application US/09864761
: Patent No. US20020948763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Ranzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENE DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: ELITE REFERENCE: Acemich-X.1
: CURRENT APPLICATION NUMBER: US 09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 09/192,412
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 09/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/652,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 09/236,459
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 48
: LENGTH: 448
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC095972.2
: OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.7
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.9
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.9
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.7
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.6
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4

```

Tue Dec 31 14:03:14 2002

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 15
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 5.1
 OTHER INFORMATION: EXPRESSED IN HB100, SIGNAL - 6.4
 US-09-864-761-48

Alignment Scores:
 Pred. No.: 2,54e-116 Length: 448
 Score: 124.00 Matches: 124
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60.49% Indels: 0
 DB: 10 Gaps: 0

US-09-727-770-2 (1-205) x US-09-964-761-48 (1-448)

QY 1 MetSerAsnSerProGluTyrAlaIleuValDheThrIleSorGlyAlaMetAlaThr 20
 DB 76 ATGTCCAAACAAACAGCGCGAGTATGCTTTGTTTCACCAATCTGGGTGCTATGGCCACC 135
 QY 21 MetValSerSerGlyLeuGlyAlaAlaCysCysMetAlaGlyAsnGlyThrGlyIleMet 40
 DB 146 ATGCTCTCCAGTGGCGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 195
 QY 41 AlaMetSerValMetTrpProGluLeuIleHisMetIlySerIleIleProValIleMet 60
 DB 196 GGCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 255
 QY 61 AlaGlyIleIleThrIleTyrClyLeuValAlaAlaValProProAlaAsnSerLeuAsn 80
 DB 256 GCTGGTATCATCAGCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 315
 QY 81 AspAsnAsnSerLeuTyrSerSerPheLeuGlyLeuGlyAlaGlyLeuGlyLeuAla 100
 DB 416 GATGACAAACAGTCTCTATAGCAGTTTCTTCAGCTGGCGCTGCGCTGAGTGGCTGCA 375
 QY 101 AlaGlyPheAlaIleValIleValIleValIleValIleValIleValIleValIleVal 120
 DB 476 GCGGCTTGGCAGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 435
 QY 121 ArgLeuPheVal 124
 DB 436 CGACTATTGTGA 447

RESULT 5
 US-09-925-401-49
 : Sequence 49, Application US/09925401
 : Patent No. US20020052408A1
 : GENERAL INFORMATION:
 : APPLICANT: Rosen et al.
 : TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 : FILE REFERENCE: PA106
 : CURRENT APPLICATION NUMBER: US/09925401
 : CURRENT FILING DATE: 2001-08-10
 : PRIOR APPLICATION NUMBER: PCT/US00/05482
 : PRIOR FILING DATE: 2000-03-08
 : PRIOR APPLICATION NUMBER: 69/124,270
 : PRIOR FILING DATE: 1999-03-12
 : NUMBER OF SEQ ID NOS: 1694
 : SOFTWARE: Patent In Ver. 2.0
 : SEQ ID NO 49
 : LENGTH: 956
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (37)
 : OTHER INFORMATION: n equals a,l,q, or c
 : NAME/KEY: misc_feature
 : LOCATION: (352)
 : OTHER INFORMATION: n equals a,l,q, or c
 : US-09-925-401-49

Alignment Scores:

Pred. No.: 2,92e-08 Length: 956
 Score: 17.00 Matches: 17
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.29% Indels: 0
 DB: 10 Gaps: 0

US-09-727-770-2 (1-205) x US-09-925-401-49 (1-956)

QY 117 AlaGlnProArgLeuPheValGlyMetIleLeuIleLeuIlePheAla 144
 DB 521 GCCCAGCAGCGCGAGTATGCTGGGCAATGATGCTGATGCTGATGCTGATGCTGATG 571

RESULT 6

US-09-887-576-814

: Sequence 814, Application US/09887576
 : Patent No. US20020144047A1
 : GENERAL INFORMATION:
 : APPLICANT: Budworth, P.
 : APPLICANT: Brown, D.
 : APPLICANT: Chang, H.
 : APPLICANT: Zhu, T.
 : APPLICANT: Han, B.
 : APPLICANT: Wang, X.
 : APPLICANT: Cooper, Bret
 : TITLE OF INVENTION: Promoters for regulation of plant expression
 : FILE REFERENCE: 1360.001US1
 : CURRENT APPLICATION NUMBER: US/09987576
 : CURRENT FILING DATE: 2001-06-25
 : PRIOR APPLICATION NUMBER: US 60/213,848
 : PRIOR FILING DATE: 2000-06-23
 : PRIOR APPLICATION NUMBER: US 60/214,087
 : PRIOR FILING DATE: 2000-06-23
 : PRIOR APPLICATION NUMBER: US 60/258,662
 : PRIOR FILING DATE: 2000-12-29
 : NUMBER OF SEQ ID NOS: 875
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 814
 : LENGTH: 498
 : TYPE: DNA
 : ORGANISM: Oryza sativa
 : US-09-887-576-814

Alignment Scores:

Pred. No.: 0.00171 Length: 498
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.85% Indels: 0
 DB: 10 Gaps: 0

US-09-727-770-2 (1-205) x US-09-487-576-814 (1-498)

QY 122 IopPheValGlyMetIleLeuIleLeuIlePheAla 144
 DB 388 GTTTTGTGGGCAATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 424

RESULT 7

US-09-887-576-815

: Sequence 815, Application US/09887576
 : Patent No. US20020144047A1
 : GENERAL INFORMATION:
 : APPLICANT: Budworth, P.
 : APPLICANT: Brown, D.
 : APPLICANT: Chang, H.
 : APPLICANT: Zhu, T.
 : APPLICANT: Han, B.
 : APPLICANT: Wang, X.
 : APPLICANT: Cooper, Bret
 : TITLE OF INVENTION: Promoters for regulation of plant expression
 : FILE REFERENCE: 1360.001US1
 : CURRENT APPLICATION NUMBER: US/09987576
 : CURRENT FILING DATE: 2001-06-25

```

: PRIOR APPLICATION NUMBER: US 60/214,848
: PRIOR FILING DATE: 2000-06-24
: PRIOR APPLICATION NUMBER: US 60/214,087
: PRIOR FILING DATE: 2000-06-24
: PRIOR APPLICATION NUMBER: US 60/258,692
: PRIOR FILING DATE: 2000-12-29
: NUMBER OF SEQ ID NOS: 875
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 815
: LENGTH: 498
: TYPE: DNA
: ORGANISM: Oryza sativa
US-09-887-576-815

```

```

Alignment Scores:
Pred. No.: 0.00171
Score: 12.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.85%
Indels: 0
Gaps: 0

```

US 09 727 770-2 (1-205) x US 09 887-576-815 (1-498)

```

QY 122 LeupheValGlyMetIleLeuIleLeuIlePheAla 133
|||||
DB 388 GTGTTGGTGAATGATCTTCATCTTCATTTTTCGC 423

```

RESULT 8

```

: Sequence 775, Application US/09887576
: Patent No. US20020144047A1
: GENERAL INFORMATION:
: APPLICANT: Budworth, P.
: APPLICANT: Brown, D.
: APPLICANT: Chang, H.
: APPLICANT: Zhu, T.
: APPLICANT: Han, B.
: APPLICANT: Wang, X.
: APPLICANT: Cooper, Bret
: TITLE OF INVENTION: Promoters for regulation of plant expression
: FILE REFERENCE: 1360.001US1
: CURRENT APPLICATION NUMBER: US 09/887-576
: CURRENT FILING DATE: 2001-06-25
: PRIOR APPLICATION NUMBER: US 60/214,087
: PRIOR FILING DATE: 2000-06-24
: PRIOR APPLICATION NUMBER: US 60/214,087
: PRIOR FILING DATE: 2000-06-24
: PRIOR APPLICATION NUMBER: US 60/258,692
: PRIOR FILING DATE: 2000-12-29
: NUMBER OF SEQ ID NOS: 875
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 775
: LENGTH: 500
: TYPE: DNA
: ORGANISM: Oryza sativa
US-09-887-576-775

```

```

Alignment Scores:
Pred. No.: 0.00171
Score: 12.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.85%
Indels: 0
Gaps: 0

```

US-09-727-770-2 (1-205) x US-09-887-576-775 (1-500)

```

QY 122 LeupheValGlyMetIleLeuIleLeuIlePheAla 133
|||||
DB 391 TTGTTGGTGAATGATCTTCATCTTCATTTTTCGC 426

```

RESULT 9

```

US-09-948-842A-645
: Sequence 645, Application US/09948842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Krops, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: FILE REFERENCE: SCRIPT400-3
: CURRENT APPLICATION NUMBER: US 09/948-842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 645
: LENGTH: 501
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-948-842A-645

```

```

Alignment Scores:
Pred. No.: 0.00172
Score: 12.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.85%
Indels: 0
Gaps: 0

```

US-09 727 770-2 (1-205) x US-09 948-842A 645 (1-501)

```

QY 122 LeupheValGlyMetIleLeuIleLeuIlePheAla 133
|||||
DB 391 CTGTTGGTGAATGATCTTCATCTTCATTTTTCGC 426

```

RESULT 10

```

US-09-887-576-786
: Patent No. US20020144047A1
: GENERAL INFORMATION:
: APPLICANT: Budworth, P.
: APPLICANT: Brown, D.
: APPLICANT: Chang, H.
: APPLICANT: Zhu, T.
: APPLICANT: Han, B.
: APPLICANT: Wang, X.
: APPLICANT: Cooper, Bret
: TITLE OF INVENTION: Promoters for regulation of plant expression
: FILE REFERENCE: 1360.001US1
: CURRENT APPLICATION NUMBER: US/09/887,576
: CURRENT FILING DATE: 2001-06-25
: PRIOR APPLICATION NUMBER: US 60/214,848
: PRIOR FILING DATE: 2000-06-24
: PRIOR APPLICATION NUMBER: US 60/214,087
: PRIOR FILING DATE: 2000-06-24
: PRIOR APPLICATION NUMBER: US 60/258,692
: PRIOR FILING DATE: 2000-12-29
: NUMBER OF SEQ ID NOS: 875
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 786
: LENGTH: 544
: TYPE: DNA
: ORGANISM: Oryza sativa
US-09-887-576-786

```

```

Alignment Scores:
Pred. No.: 0.00185
Score: 12.00
Length: 543
Matches: 12

```

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.85%	Indels:	0
DB:	10	Gaps:	0

US-09-727-770-2 (1-205) x US-09-887-576-786 (1-543)

yy 122 LeuPheValGlyMetIleLeuIleLeuIlePheAla 133
 |||||
 bb 389 GTGTCTGTCGGATGATCTCATCTCATCTCTGGCC 424

RESULTS

```

US 09-770-149-324
: Sequence 324, Application US/09770149
: Patent No. US20020059663A1
: GENERAL INFORMATION:
: APPLICANT: Gorlach, Jorn
: APPLICANT: An, Yong-Qiang
: APPLICANT: Hamilton, Carol M.
: APPLICANT: Price, Jennifer L.
: APPLICANT: Raines, Tracy M.
: APPLICANT: Yu, Yang
: APPLICANT: Ramezka, Joshua G.
: APPLICANT: Page, Amy
: APPLICANT: Matthew, Abraham V.
: APPLICANT: Ledford, Brooke L.
: APPLICANT: Woessner, Jeffrey P.
: APPLICANT: Haas, William David
: APPLICANT: Garcia, Carlos A.
: APPLICANT: Krickor, Maja
: APPLICANT: Slader, Ted
: APPLICANT: Davis, Keith K.
: APPLICANT: Allen, Keith
: APPLICANT: Hofman, Neil
: APPLICANT: Harban, Patrick

```

NOTICE TO CONTRIBUTORS: PLEASE SUBMIT ALL MANUSCRIPTS TO THE EDITORIAL BOARD OF THE JOURNAL OF THE AMERICAN SOCIETY OF CLIMATE ENGINEERS.

```

? TITLE OF INVENTION: thaliana
? FILE REFERENCE: 2024 (EANA-014PRV)
? CURRENT APPLICATION NUMBER: US/09/770,149
? CURRENT FILING DATE: 2001-01-26
? PRIOR APPLICATION NUMBER: 60/178,506
? PRIOR FILING DATE: 2000-01-27
? NUMBER OF SEQ ID NOS: 999
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 323
? LENGTH: 686
? TYPE: DNA
? ORGANISM: Arabidopsis thaliana
? S-09-770-149-323

```

Alignment Scores:	
Pred. No.:	0.00231
Score:	12.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	5.85%
DB:	10
Length:	686
Matches:	12
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-727-770-2 (1-205) x US-09-770-149-323 (1-686)

Q7 122 LoughicValGlyMetLeuLuuLeuLeuPheAla 133
 ffffffffffffd

D6 408 TTGGTCTGGGAATGCATTTCACGTCTGT 443

RESULT 12

```

US-09-887-456-466.
; Sequence 466, Application US/09887576
; Patent No. US2002014047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.

```

```

? APPLICANT: Han, B.
? APPLICANT: Wang, X.
? APPLICANT: Cooper, Bret
? TITLE OF INVENTION: Promoters for regulation of plant expression
? FILE REFERENCE: 1360.001US1
? CURRENT APPLICATION NUMBER: US/09/0947, 676
? CURRENT FILING DATE: 2001-06-25
? PRIOR APPLICATION NUMBER: US 60/213,848
? PRIOR FILING DATE: 2000-06-23
? PRIOR APPLICATION NUMBER: US 60/214,987
? PRIOR FILING DATE: 2000-06-23
? PRIOR APPLICATION NUMBER: US 60/258,492
? PRIOR FILING DATE: 2000-12-29
? NUMBER OF SEQ ID NOS: 875
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 466
? LENGTH: 805
? TYPE: DNA
? ORGANISM: Arabidopsis thaliana
? S.-09-887-576-466

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Alignment Scores:			
Prod. No.:	0, 00269	Length:	805
Score:	12, 00	Matches:	12
Percent Similarity:	100, 00%	Conservative:	0
Best Local Similarity:	100, 00%	Mismatches:	0
Query Match:	5, 85%	Indels:	0
DB:	10	Gaps:	0

$$115-116-737-770 \rightarrow 11-105) \times (12-04-887-576-466) \rightarrow 1806)$$

Q7	122	Leu	He	Val	Leu	Met	Leu	Leu	Leu	Leu	Ala	133
Q8	495	Cys	Ala	Trp	Val	Met	Val	Val	Val	Val	Ala	740

2015-11-12

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> US-09-770-445-683
> Sequence 683, Application US/09770445
> Patent No. US2002052281A1
> GENERAL INFORMATION:
> APPLICANT: Gorlach, Jörn
> APPLICANT: An, Yong-Qiang
> APPLICANT: Hamilton, Carol M.
> APPLICANT: Price, Jennifer L.
> APPLICANT: Raines, Tracy M.
> APPLICANT: Yu, Yang
> APPLICANT: Rameeka, Joshua G.
> APPLICANT: Page, Amy
> APPLICANT: Matthew, Abraham V.
> APPLICANT: Ledford, Brooke L.
> APPLICANT: Woessner, Jeffrey P.
> APPLICANT: Haas, William David
> APPLICANT: Garcia, Carlos A.
> APPLICANT: Krieger, Maja
> APPLICANT: Slader, Ted
> APPLICANT: Davis, Keith R.
> APPLICANT: Allen, Keith
> APPLICANT: Hoffman, Neil
> APPLICANT: Hurlan, Patrick
> TITLE OF INVENTION: Expressed Sequences of Arabidopsis
> FILE REFERENCE: thaliana (PARA 012PRV)
> CURRENT APPLICATION NUMBER: US-2002-0776445
> CURRENT FILING DATE: 2001-01-26
> PRIOR APPLICATION NUMBER: US-60/179,472
> PRIOR FILING DATE: 2000-01-27
> NUMBER OF SEQ ID NOS: 999
> SOFTWARE: FastSeq for Windows Version 4.0
> SEQ ID NO 683
> LENGTH: 834
> TYPE: DNA
> ORGANISM: Arabidopsis thaliana
> US-09-770-445-683

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1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text outlines various methods for organizing and storing records, including digital databases and physical filing systems. It also mentions the need for regular audits and reviews to ensure the integrity of the data.

2. The second part of the document focuses on the role of communication in achieving organizational goals. It highlights the importance of clear and concise communication, both internally and externally. The text provides guidelines for effective communication, such as using appropriate language, listening actively, and providing feedback. It also discusses the benefits of open communication, including improved collaboration and faster decision-making.

3. The third part of the document addresses the issue of risk management. It defines risk as the potential for loss or damage and explains how to identify, assess, and mitigate risks. The text provides a framework for risk management, including the identification of risks, the assessment of their likelihood and impact, and the implementation of control measures. It also discusses the importance of monitoring and reviewing risks over time.

4. The fourth part of the document discusses the importance of training and development. It emphasizes that ongoing training and development are essential for maintaining a skilled and motivated workforce. The text outlines various training methods, including classroom instruction, on-the-job training, and self-directed learning. It also discusses the importance of setting learning objectives and evaluating the effectiveness of training programs.

5. The fifth part of the document discusses the importance of innovation and creativity. It emphasizes that innovation and creativity are essential for staying competitive in a rapidly changing market. The text provides guidelines for fostering innovation and creativity, such as encouraging open-mindedness, providing resources for experimentation, and rewarding creative ideas. It also discusses the importance of protecting intellectual property and managing innovation risks.

6. The sixth part of the document discusses the importance of sustainability. It defines sustainability as the ability to meet the needs of the present without compromising the ability of future generations to meet their own needs. The text outlines various sustainability initiatives, including environmental protection, social responsibility, and economic development. It also discusses the importance of measuring and reporting on sustainability performance.

7. The seventh part of the document discusses the importance of ethics and governance. It emphasizes that ethics and governance are essential for building trust and credibility. The text provides guidelines for ethical behavior, such as being honest, transparent, and fair. It also discusses the importance of establishing a strong governance structure and implementing effective controls.

8. The eighth part of the document discusses the importance of customer service. It emphasizes that excellent customer service is essential for retaining customers and attracting new ones. The text provides guidelines for providing excellent customer service, such as listening to customer feedback, resolving complaints quickly, and going above and beyond to meet customer needs. It also discusses the importance of training customer service staff and monitoring customer satisfaction.

9. The ninth part of the document discusses the importance of financial management. It emphasizes that sound financial management is essential for the long-term success of any organization. The text outlines various financial management practices, including budgeting, forecasting, and financial reporting. It also discusses the importance of maintaining accurate financial records and seeking professional advice when needed.

10. The tenth part of the document discusses the importance of strategic planning. It emphasizes that strategic planning is essential for setting clear goals and determining the best way to achieve them. The text provides guidelines for developing a strategic plan, such as conducting a SWOT analysis, setting SMART goals, and implementing a strategic action plan. It also discusses the importance of reviewing and updating the strategic plan regularly.

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text outlines various methods for organizing and storing data, including digital databases and physical filing systems. It also mentions the need for regular audits and reviews to ensure the integrity of the information.

2. The second section focuses on the role of communication in achieving organizational goals. It highlights the importance of clear and concise communication channels, both internally and externally. The text suggests implementing regular meetings and reports to keep all stakeholders informed and engaged. It also discusses the benefits of open communication in fostering a collaborative work environment and resolving conflicts effectively.

3. The third part of the document addresses the challenges of managing resources efficiently. It notes that organizations often face constraints in terms of budget, time, and personnel. To overcome these challenges, the text recommends prioritizing tasks and projects based on their strategic importance. It also suggests leveraging technology and automation to streamline processes and reduce manual errors. Additionally, it emphasizes the importance of continuous learning and skill development for the workforce to adapt to changing market conditions.

4. The final section discusses the importance of maintaining a strong corporate culture. It argues that a positive and values-driven culture is crucial for attracting and retaining top talent. The text suggests that leadership should model the desired behaviors and values, and encourage employees to do the same. It also mentions the importance of recognizing and rewarding employees for their contributions, which can boost morale and productivity. Finally, it stresses the need for a culture of innovation and risk-taking, where employees feel empowered to propose new ideas and solutions.

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2. The second section focuses on the role of communication in achieving organizational goals. It highlights the importance of clear and concise communication channels, both internally and externally. The text suggests implementing regular meetings and reports to keep everyone informed and aligned. It also discusses the benefits of open communication, such as improved collaboration and faster problem-solving. The section concludes by stressing the need for a strong communication culture where everyone feels encouraged to share ideas and feedback.

3. The third part of the document addresses the challenges of managing a large and diverse team. It acknowledges that different team members may have varying skills, experiences, and backgrounds, which can lead to misunderstandings and conflicts. The text provides strategies for managing these differences, such as assigning tasks based on individual strengths and providing ongoing training and support. It also emphasizes the importance of setting clear expectations and deadlines to ensure that the team is working towards common objectives. The section ends by encouraging leaders to foster a supportive and inclusive environment where team members can thrive.

4. The final section discusses the importance of continuous learning and improvement. It notes that in a rapidly changing world, organizations must stay up-to-date with the latest trends and technologies. The text suggests investing in employee development through workshops, seminars, and online courses. It also mentions the value of seeking feedback from customers and stakeholders to identify areas for improvement. The section concludes by stating that a commitment to learning and growth is essential for long-term success and competitiveness.

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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 16890
LENGTH: 612
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005973.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.9
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5
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US-09-864-761-16890

Query Match          96.7%; Score 612; DB 10; Length 612;
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Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text outlines various methods for organizing and storing data, including digital databases and physical filing systems. It also mentions the need for regular audits and reviews to ensure the integrity of the information.

2. The second section focuses on the role of communication in achieving organizational goals. It highlights the importance of clear and concise communication, both internally and externally. The text provides examples of effective communication strategies, such as regular team meetings, open-door policies, and the use of various communication channels like email, phone, and face-to-face interactions. It also discusses the importance of listening and understanding the needs and concerns of all stakeholders.

3. The third part of the document addresses the challenges of managing a large and diverse workforce. It discusses the importance of providing ongoing training and development opportunities to ensure that employees have the skills and knowledge needed to perform their jobs effectively. The text also touches on the importance of creating a positive work environment that fosters collaboration and innovation. It mentions the need for flexible work arrangements and the importance of recognizing and rewarding employee achievements.

4. The final section discusses the importance of staying up-to-date with the latest trends and technologies in the industry. It emphasizes that continuous learning and innovation are key to long-term success. The text provides examples of how organizations can stay ahead of the curve by investing in research and development, attending industry conferences, and collaborating with external partners. It also mentions the importance of having a clear vision and strategy for the future.

